

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 20, 2002, 08:42:08 ; Search time 223.75 Seconds  
(without alignments)  
254.911 Million cell updates/sec

Title: US-08-212-185-12

Perfect score: 770

Sequence: 1 MAQNQLQQLDTRYLKLQHLQ.....QFESLTFDMLTSECATSPM 770

Scoring table:

Gapop 60.0 , Gapext 60.0

Search:d: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

1: /SIDSL/gcgdata/geneseq/AA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/AA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/AA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/AA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/AA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/AA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/AA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/AA1987.DAT.\*  
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10: /SIDSL/gcgdata/geneseq/AA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/AA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/AA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/AA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/AA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/AA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/AA1995.DAT.\*  
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18: /SIDSL/gcgdata/geneseq/AA1997.DAT.\*  
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21: /SIDSL/gcgdata/geneseq/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	100.0	770	16	Mouse Stat3 (19sf6
2	770	100.0	770	17	Mouse STAT4, Mus
3	568	73.8	770	21	N-terminal domain
4	532	69.1	770	20	Human STAT3 allele
5	532	69.1	793	21	Lung cancer associ
6	442	57.4	770	16	Mouse liver acute
7	393	51.0	393	22	Mouse Stat3 protei
8	271	35.2	271	22	Mouse Stat3 protei
9	252	32.7	252	22	Mouse Stat3 protei
10	236	30.6	236	22	Mouse Stat3 protei
11	229	29.7	229	22	Mouse Stat3 protei

12	223	29.0	223	22	AA72854	Mouse Stat3 protei
13	221	28.7	770	16	AA82993	Human placenta acu
14	221	28.7	770	22	AA819964	Human signal trans
15	213	27.7	213	22	AA72851	Mouse Stat3 protei
16	210	27.3	229	22	AA72862	Mouse Stat3 mutant
17	207	26.9	228	22	AA72861	Mouse Stat3 protei
18	207	26.9	229	22	AA72863	Mouse Stat3 mutant
19	194	25.2	229	22	AA72860	Mouse Stat3 protei
20	185	24.0	185	22	AA72855	Mouse Stat3 protei
21	176	22.9	176	22	AA72848	Mouse Stat3 protei
22	154	20.0	154	22	AA72840	Mouse Stat3 protei
23	143	18.6	143	22	AA72849	Mouse Stat3 protei
24	141	18.3	141	20	AA707240	Fragment of human
25	139	18.1	173	22	AA819973	Human STAT-3 DNA b
26	138	17.9	141	20	AA707241	Fragment of mouse
27	129	16.8	129	22	AA72856	Mouse Stat3 protei
28	128	16.6	128	22	AA72852	Mouse Stat3 protei
29	112	14.5	112	17	AAW03167	Mouse STAT4 DNA bi
30	103	13.4	141	20	AAW07239	Fragment of human
31	96	12.5	96	22	AA72857	Mouse Stat3 protei
32	95	12.3	95	22	AA72853	Mouse Stat3 protei
33	22	2.9	22	22	AA73232	Stat3 SH2 domain C
34	14	1.8	14	21	AA812847	STAT3 tyrosine pho
35	12	1.6	12	17	AA894426	STAT3 peptide, Ser
36	12	1.6	107	22	AA819971	Human STAT-1 SH2 d
37	12	1.6	376	22	AA72845	Mouse Stat1 protei
38	12	1.6	582	19	AAW62996	Human truncated St
39	12	1.6	701	14	AA841335	84 kD ISGF-3alpha.
40	12	1.6	712	16	AA72079	Human Stat84, Hom
41	12	1.6	712	17	AAW03170	Human STAT1-beta.
42	12	1.6	712	19	AAW62995	Human STAT1-beta p
43	12	1.6	739	14	AA841334	91 kD ISGF-3alpha.
44	12	1.6	749	16	AA72080	Mouse Stat1 (Stat9
45	12	1.6	749	17	AAW03172	Mouse STAT1, Mus

#### ALIGNMENTS

RESULT 1  
AAR72082  
ID AAR72082 standard; Protein; 770 AA.  
XX  
AC AAR72082;  
XX  
DT 27-SEP-1995 (first entry)  
XX  
DE Mouse Stat3 (19sf6).  
XX  
KW Signal transducer and activator of transcription; STAT; 19sf6;  
KW Stat3; receptor recognition factor; transcription factor;  
KW cellular debilitation; derangement; dysfunction;  
KW interferon-gamma.  
XX  
OS Mus sp.  
XX  
PN WO9508629-A.  
XX  
PD 30-MAR-1995  
XX  
PF 26-SEP-1994; 94WO-US10849.  
XX  
PR 24-SEP-1993; 93US-0126588.  
PR 24-SEP-1993; 93US-0126595.  
PR N-terminal domain  
PR 11-MAR-1994; 94US-0212184.  
PR 11-MAR-1994; 94US-0212185.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Darneil JE, Schindler CW, Shuai K, Wen Z, Zhong Z;  
XX WPI: 1995-139598/18.  
DR N-PSDB; AAQ89340.

XX Receptor recognition factor implicated in transcriptional  
PT stimulation of genes - useful in drug screening assays and/or  
PT for treating cellular debilitations, derangements and/or  
PT dysfunctions, etc.  
XX  
PS Claim 1; Page 107-110; 160pp; English.  
XX  
CC A fragment encoding the human Stat91 protein was used to screen a  
CC murine thymus and spleen cDNA for homologous proteins. A highly  
CC homologous gene (given in AA089338) was isolated that encoded a  
CC 91 kDa protein (AA072080) (Stat1) that was responsive to interferon-  
CC gamma. Using a fragment of the mouse gene as probe, 2 additional  
CC members of the 113-91 family of receptor recognition factor  
CC proteins were isolated. The 2 genes (AA089339-40) were cloned  
CC in plasmids 13srl and 19s16 and encoded proteins termed Stat4  
CC (AA072081) and Stat3 (AA072082), respectively.  
XX  
SQ Sequence 770 AA;

Query Match 100.0%; Score 770; DB 16; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MAQWNLQLOLDTRYLKHOLYSDTFPMELOFLAPWIESODWAYAASKESHATLVFHNL 60  
Db 1 maqwnqlqldtrylkqhlqysdtfpmelrqflapwiesqdwayaaskeshatlvfhn 60  
Oy 61 LGEIDDOQYSRFLQSNVLYOHNLRRIRKOFLOSRYLEKPMELIARIVARCLWEESRLLOTA 120  
Db 61 lgeidqqysrflqsnvlyqhnrrirkqlqsyrylekpmeiarivarclweesrlloqtaa 120  
Oy 121 TAAQGGGANHTPAAYTEKQOMLEQHLQDVRRKRVQDLEQRMKVVENLQDDDFNYKTLK 180  
Db 121 taaggqganhtpaayteqomleqhlqdvrrkrvqdleqrmkvvenlqdddfnyktlk 180  
Oy 181 SQGDMQDLNGNQSVTROKMOQLTALDOMRRSTVSELAGLSAMEYVQKTLTDEEL 240  
Db 181 sqgdmqdlngnqsvtqkmoqltaldomrrstvselaglsameyvqkltdeel 240  
Oy 241 ADWRRRPIACIGPPNICDLRLENWITSLSAESQLOTRQOIKLEELQKVSXKGDPIVQ 300  
Db 241 adwrrrpiaci gppnicdlrlenwitslsaesqltrqoikleelqkvsvxkgdpivq 300  
Oy 301 HRPMLEERIVELFNLKMSAFVVERQPCMPHDPRLVIKTCYQVTTKVRLLYKFPPELNY 360  
Db 301 hrpmleerivelfnlkmsafvverqpcmp hdp rlviktgyqftckvrllykfpelny 360  
Oy 361 OLKIKVCIDKSDGVAALRGSRKFNILGTNTKVMNMEESNNGSLSAFFKHLTLREORCGN 420  
Db 361 qlkikvcidksgdvaalrgsrkfnilgtntkvmnmeesnngslsaefkhltlreorcgn 420  
Oy 421 GGRANDASLIIVTEELHLITFETEVYHOGJLKIDLETHSLPWWVINSNTQMPNAWA:ILWY 480  
Db 421 ggrandasliivteelhlitfetevyhogglikidletshslpwwvlnsnicqmpnawasilwy 480  
Oy 481 NMLTNNPKNVNFFTKPPIGTWQDVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540  
Db 481 nmltnnpkvnfftkppigtwdqvaevlwsqfsssttkrglsieqlttlaekllpggvny 540  
Oy 541 GCQITWAKFCCKENMAGKGFSSFWNLDMIIDLVKKYILALWNEGYIMGFISKERERAILST 600  
Db 541 qcqitwakfckenmagkgfssfwwnldm iidl vkkylalwnegyimgfiskereraillst 600  
Oy 601 KPPGTFLLRFSRSKEGCVFTTWKEDISCKTOIQSVEPYTKKOOLNNMSPAEIIMGYKIM 660  
Db 601 kppgtfllrfsrskegcvfttwekdisgktqisvpytkkqolnnmsfaeiiimgykim 660  
Oy 661 DATNILVSPVLVLPDIPKPEAFGKYCRPESQEPHADPGSAAPYLKTKFCVPTPTCSN 720  
Db 661 datnilvspvlvlpdipkpeafgkycrpesqehpeadpgsaapylktkfcvptptcsn 720

Oy 721 TIDPMSPTLDSLMOFGNNGEAGPSAGGOFESLTFDMDLTSECATSPM 770  
Db 721 tidpmsptl dslmqfgnnggeagsaggqfesi t fmdltsecatspm 770  
RESULT 2  
AAW03176  
ID AAW03176 standard; Protein; 770 AA.  
XX  
AC AAW03176;  
XX  
DT 24-OCT-1996 (first entry)  
XX  
DE Mouse STAT4.  
XX  
KW STAT4; signal transducer and activator of transcription;  
KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;  
KW autoimmune disease; antagonist; therapy.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Domain 398..508  
FT /label= DNA\_binding\_domain  
FT /note= "Claim 3, page 110"  
XX  
PN W09620954-A2.  
XX  
PD 11-JUL-1996.  
XX  
PF 28-DEC-1995; 95WO-US17025.  
XX  
PR 06-JAN-1995; 95US-0369796.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Darnell JE, Horvath CM, Wen Z, Zhong Z;  
XX  
DR WPI: 1996-333941/33.  
DR N-PSDB: AAT31280.  
XX  
New STAT protein DNA-binding domain peptide(s) - useful for  
diagnosing, preventing or treating cellular dysfunction, e.g.  
oncogenesis, inflammation, parasitic disease or autoimmunity  
XX  
PS Disclosur-; Page 87-90; 138pp; English.  
XX  
CC Mouse signal transducer and activator of transcription (STAT)  
CC protein STAT4 (AAW03176) serves a dual purpose, i.e. signal  
CC transduction from ligand-activated receptor kinase complexes  
CC followed by nuclear translocation and DNA binding to activate  
CC transcription. Recombinant STAT4 can be obtd. using cDNA clone  
CC 19s16 (AAT31278) obtd. from splenic/thymic cells. STAT4 includes  
CC a DNA-binding domain (see also AAW03167) capable of both  
CC receptor recognition and message delivery via DNA binding in a  
CC receptor-ligand specific manner. STAT proteins and their DNA  
CC binding domains (see also AAW03165-75) are useful for screening  
CC antagonists used to inhibit STAT-mediated signal transduction  
CC and activation of transcription.  
XX  
SQ Sequence 770 AA;  
Query Match 100.0%; Score 770; DB 17; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MAQWNLQLOLDTRYLKHOLYSDTFPMELOFLAPWIESODWAYAASKESHATLVFHNL 60  
Db 1 maqwnqlqldtrylkqhlqysdtfpmelrqflapwiesqdwayaaskeshatlvfhn 60  
Oy 61 LGEIDDOQYSRFLQSNVLYOHNLRRIRKOFLOSRYLEKPMELIARIVARCLWEESRLLOTA 120  
Db 61 lgeidqqysrflqsnvlyqhnrrirkqlqsyrylekpmeiarivarclweesrlloqtaa 120

FT	Region	43..47	/label= "Alpha helix 5"
FT	Region	50..73	/label= "Alpha helix 6"
FT	Region	77..96	/label= "Alpha helix 7"
FT	Region	99..119	/label= "Alpha helix 8"
XX	US087478-A.		
PN	XX		
PD	11-JUL-2000.		
XX	XX		
PF	23-JAN-1998;	98US-0012710.	
PR	23-JAN-1998;	98US-0012710.	
XX	(UVRQ ) UNIV ROCKEFELLER.		
XX	Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;		
XX	WPI: 2000-505108/45.		
XX	New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development -		
PT	PT		
PT	PT		
XX	Disclosure; Fig 1; 42pp; English.		
XX	XX		
CC	The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of atomic coordinates of the N-terminal domain to a resolution of greater than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal.		
XX	Sequence	770 AA;	
QY	Query Match	73.8%;	Score 568; DB 21; Length 770;
	Best Local Similarity	99.7%;	Pred. No. 0;
	Matches 768; Conservative	0; Mismatches	2; Indels 0; Gaps
QY	1	MAOWNOIQQIDTRYIKOIHQIYSDTFPMEILRQFLAPWIESQDWAYAASKESHATLVFHNL 60	
Db	1	maqwnqlqiddtrylkqlhqlysdtfmeilrqlflapwiesqsdwayaaskeshativfhnl 60	
QY	61	LGEIDQOYSRFLOESNVLVYOHNNLRRIKQFTQSRYLEKPMETARIACRLWESRLQATA 120	
Db	61	lgeidqqysrflgesnvlvydhnmlrrikqfllqsrlylekpmearivarcilweesrlilqtaa 120	
QY	121	TAAQGGQGANHPTAAVYTEKQOMLEOHLQDVRKRVQDLEOKMKVVENIQDDFDNFVKTLLK 180	
Db	121	taaqggqganhptaavvtekkqmqleqlhldqvrkrvqdeqmkkvvenlqqddfdnfyktllk 180	
QY	181	SQGMQDLNGNNSVTRQKMOOILEQMIITALIDQMRRSIVSEILSAMYVYOKTILDEEL 240	
Db	181	sqgdmqdlngundsvtrqknqleqmlitalidqmrrsvsvelaglsameyvqktlldeel 240	
QY	241	ADMKRREPEIACIGPPNICIDRLNENITSLAESOLOTRQOIKKLEELQOKVSKGDPVQ 300	
Db	241	admrtrqieaciagppnicidrlnenwitslaesqlqltrqikkleclqkvsvykgdpivq 300	
QY	301	HRPMLERIVELFRNLWKMSAFVVERQCPMHPDRPLVIKTGVQFTTKVKRLIAWKFPPELNY 360	
Db	301	hrpmlerivelfrnlkmsafvverqcpmhpdrplvlklqvqflltkvrllvklpelny 360	
QY	361	QIKIKVCIDKSGDVAALRGSRKFNITLGTNTKVMNPFESNNGSLSAFFPKHITLREORCGN 420	

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DB 361 qlkikvcidkugdvaaigrskkniilgtntkvmmeesnngsisaefkhltlreqrcgn 420  
QY 421 GGRANCASLIVTEELHLLITETETEVYHGLKTDLETHSLPVVVISNICOMPNAWASILWY 480  
DB 421 ggrancdaslivteelhlitfetevehgdkidtechslpvvvisnicompnaasilw 480  
QY 481 NMLTNNPKNVNFTKPPICGTWDOVAEVLWSQFSSTTKRGLSTIEQJTTTAEKLLGPGVWYS 540  
DB 481 nmltnpknvnfkppigtwdqvaevlswqfssttkrglsieqittlaekllpgvwnys 540  
QY 541 GCOITWAKFCKENACKGFSFWWLDNIIDLKYLALWNEGYIMGFTSKRERAILST 600  
DB 541 gcqitwakfckenackgfsfwwldnidlvlkylalwnegyimgfiskerailst 600  
QY 601 KPPCTELLRFSSSSKEGGVTFVWEKDISGKTQIOSVEPYTKQOLNNMSFAEIMGYKIM 660  
DB 601 kppgtellrfsssskeggvtfvwekdlsqktqigsvepytkqolnnmsfaelimgykim 660  
QY 661 DATNILVSLVLYLPDIKPEBAFGKYCRPESQEHPEADPGSAAPYLKTKFKICVTPTTCSN 720  
DB 661 datnilvslvlylpdikpebafgkycrpesqehpeadpgsaapyiktkfkicvtpttcsn 720  
QY 721 TIDLPMSPRTLDSLMQFGNNGGAEPGAGQFESLTFDMDLTSECATSPM 770  
DB 721 tidlpmsprtlslmqfgnnggaepsaggqfsltfddmiltsecatspm 770  
RESULT 4  
AAV03768  
ID AAV03768 standard; Protein; 770 AA.  
XX AC AAY03768;  
XX DT 11-JUN-1999 (first entry)  
XX DE Human STAT3 allelic variant.  
XX KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;  
KW intracellular transcription factor; interleukin-6; medicament; variant;  
KW pharmaceutical; autoimmune disease; inflammatory; human.  
OS Homo sapiens.  
PN EP905234-A2.  
XX 31-MAR-1999.  
XX 18-FEB-1998; 98EP-0102774.  
XX 16-SEP-1997; 97EP-0116061.  
XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
XX Della Pietra L, Serlupi-Crescenzi O;  
XX WPI; 1999-192664/17.  
XX N-PSDB; AAX29281.  
XX New human Signal Transducer and Activator of Transcription 3 (STAT3)  
XX allelic variant useful for treatment of autoimmune and inflammatory  
XX disease  
XX Claim 2; Page 9-13; 32pp; English.  
XX The present sequence represents a predominant allelic variant of human  
XX Signal Transducer and Activator of Transcription 3 (STAT3) protein, an  
XX intracellular transcription factor which mediates IL-6 signals. The  
XX encoding sequence differs from the original published human STAT3 gene  
XX sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3  
XX DNA molecule can be used for the recombinant expression of the variant.  
XX STAT3 protein is useful as a medicament or pharmaceutical composition for  
XX treatment of autoimmune or inflammatory diseases.

SO Sequence 770 AA;  
Query Match 69.1%; Score 532; DB 20; Length 770;  
Best Local Similarity 59.7%; Pred. No. 0;  
Matches 732; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 26 FPMELRQFLAPWIESODMAYAAKESHATLVFHNLLIGLIEUQOYSRFLQESNVLYOHNLRR 85  
DB 26 fpmelrqflapwiesodmayaaakeshatlvfhnllgeidqysrflqesnvlyqhnllrr 85  
QY 86 IKQFLQSRYLEKPEMEIARIVARCLWEESRLLOTAATAAQOGGQANHTAAVVTKEQOMLE 145  
DB 86 ikqflqsrylekpemeiarivarcliweesrllqtaataaaggqganhtaaavvtekkqgle 145  
QY 146 QHLQDVVF KVQDLEQKMKVVENLQDDFDENFKTLKSGQMDQDLNNGNOSVTRQKMOQLEQ 205  
DB 146 qhlqdvrvrkdleqkmkvenlqddfdnfkylksqgmdqdlngnngsvtrqkmoqleq 205  
QY 206 MLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRPEIACIGGPPNICLDRIEN 265  
DB 206 mlaldqmrsvselagilsameyvvqkltldeeladwkrqgiaciaggppnicldrien 265  
QY 266 WITSIAESQLOTRQOIKKLEELOQKVSYGQDPVQHRPMLPERIVELFRNLKMSAFVVER 325  
DB 266 witsiaesqltrqqikkleeiqkvsvyqgdpivqhrpmlperivellfrnlmksafvver 325  
QY 326 OPCMPMPDRPLVKTGVQFTTKVRLLVKFPPELNTQLKIKVCIDKDSGDVAALRGRKFN 385  
DB 326 opcmphdpdrplviktgvqfttkvrlvkvfpelntyqlkikvcidkdsgdvaalrgsrkfn 385  
QY 386 ILGTNTKVMNEESNNGSLSAEFKHLTLRQRCGNGGRANCDASLIVTEELHLITFETEV 445  
DB 386 ilgtntkvmneesnngslsaefkhltlreqrcngngrancdaslivteelhlitfetev 445  
QY 446 YHGLKIDLETHTSLPVVVISNICOMPNAWASILWYNMLTNNPKNVNFTKPPIGTWQVA 505  
DB 446 yhgldkidlhtslpvvvisnicompnawasilwynmltnpknvnfckppigtwdqva 505  
QY 506 EVLSWQFSSTTKRGLSIEQJTTTAEKLLGPGVWYSQCTITWAKFKENMAGKGFSTFWWL 565  
DB 506 evlswqfssttkrglsieqittlaekllpgvwnysqctitwakfckenmagkfstfwwl 565  
QY 566 DNIIDLKVKYILALWNEGYIMGFTSKRERAILSTKPPGFTLLRFSSSSKEGGVTTTWE 625  
DB 566 dniidlvlkylalwnegyimgfiskerailstkpptgftllrfsssskeggvtttwe 625  
QY 626 KDISGKTQIOSVEPYTKQOLNNMSFAEIMGYKIMDATNILVSPLYLYLPDIKPEBAFGK 685  
DB 626 kdisgktqigsvepytkqolnnmsfaelimgykimdatnilvslplylylpdikpeaefgk 685  
QY 686 YCRPESQEHPEADPGSAAPYLKTKFKICVTPTTCSNTIDLPMSPRTLDSLMQFGNNGGA 745  
DB 686 ycrpesqehpeadpgsaapyiktkfkicvtpttcsntidlpmsprtlslmqfgnnggae 745  
QY 746 PSAGGQFESLTFDM 759  
DB 746 psaggqfsltfdm 759  
RESULT 5  
AAB58442  
ID AAB58442 standard; Protein; 793 AA.  
XX AC AAB58442;  
XX DT 14-MAR-2001 (first entry)  
XX DE Lung cancer associated polypeptide sequence SEQ ID 780.  
XX Human; lung cancer associated protein; neuroprotective; cytostatic;  
XX cardioactive; immunomodulatory; muscular active; vulnerary;  
KW gastrointestinal; nephrotropic; antineoplastic; gynecological;

KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;  
KW proliferative disorder; wound healing; infectious disease.

XX Homo sapiens.

PN WC200055180-A2.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05918.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.

XX Ruben SM;

XX WPI; 2000-587514/55.

DR N-PSDB; AAF18318.

XX Lung cancer associated gene sequences, referred to as lung cancer  
PT antigens, useful for treatment, prevention, and diagnosis of disorders  
PT such as lung cancer -

XX Claim 11; Page 1310-1313; 1425pp; English.

XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer  
CC associated proteins represented in AAF58106 - AAF58548. Lung cancer  
CC associated proteins and polynucleotide sequences, their agonists, and  
CC antagonists may have neuroprotective; cytostatic; cardioactive;  
CC immunomodulatory; muscular active general; vulnerary; gastrointestinal  
CC general; nephrotropic; antiinfective; gynecological; or antibacterial  
CC activity. The invention also includes antibodies specific for the  
CC protein or polynucleotide sequences. The lung cancer associated  
CC polynucleotide sequences may be used for detection of lung cancer,  
CC chromosome identification, as chromosome markers, and for numerous other  
CC diagnostic or research purposes. The proteins may be used to treat  
CC disorders such as neural, immune, muscular, reproductive,  
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
CC disorders. The proteins may also be used in the treatment of wounds and  
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and  
CC peptide AAF58549 are used in the course of the invention for the  
CC identification and characterisation of the polynucleotide and protein  
CC sequences.

XX Sequence 793 AA;

Query Match 69.1%; Score 532; DB 21; Length 793;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 732; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 26 FPMELRQFLAPWTESODMAYAAKESHATLVFNHNLGEIDQYSRFLQESNVLYQHNLRR 85

Db 49 fpmelrgflapwiesqgwaYaakeshatlvfnhlgeidqgysrflqesnvlyqhnlr 108

Qy 86 IKQFLQSRYLEKPMELIARIIVARCLWEESRLLOTAATAAQOQGOANHPATAAVTEKQOMLE 145

Db 109 ikqlqsrylekpmelariivarclweesrlllqtaataaqqggqanhpataavtekgqmlle 168

Qy 146 QHLDQVRKRVDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLNGNNSQSVTRKMOOLEQ 205

Db 169 qhlqdvrrkryqdleqkmmkvenlqdddfnyktlksqgdmqdlngnnsqsvtrqkmqgleq 228

Qy 206 MLTALDQMRRIIVSELAGLLSAMEYVQKTLTDELDWKRPEFACIGGPPNICLDRLN 265

Db 229 mltdldqmrriivselagllsameyvqkltldeeldwkrqqlacigggppnicldrlen 288

Qy 266 WITSLAESQLOTRQIKKLEELQOKVSKGDPVIVQHRPMLPEERIVELFRNLMSAFVVER 325

Db 289 witslaesqltrqikkleelqkvsykgdplvqhrpmlpeeriveifrnlnmsafvver 348

Qy 326 QPCMPMHFDRLPLVIKTGVOFTTKVRLIWKFPPLNYOLKIKVICDKSDGVAALRGRKFN 385  
Db 349 qpcmpmhfdrlplviktgvfttkvrlilvkfpeInlyqlkvicdkdsgdvaalrgsrkfn 408  
Qy 386 ILGTTNTKVMNMEESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEV 445  
Db 409 ilgtntkvmnmeesnngslsaefkhltlregrcngngrancdaslivteehlitfetev 468  
Qy 446 YHOGLIKIDLETHSLPVVVISNICOMPNAWASILWYNTNNTNNPKNVNFPTKPPIGTWDQVA 505  
Db 469 yhglikidlethslpvvvisnicompnawasilwynmtnnpknvnttkppigtwdqva 528  
Qy 506 EVLSWQFSSTTKRGLSIEQLFTLAKKLJGPGVNYSCQITWAKFKCKENMAGKGFSPWWWL 565  
Db 529 evlswqfssllkrglsieqlftlaekllgpgvnysgciltwakfckemmagkfstwwwl 588  
Qy 566 DNIIDLKVKYILALNKGYIMGFISKERERAILSTKPGCTFLLRFSESSKEGVTFTWYE 625  
Db 589 dnildlvkylialwnegyimgfiskereralistkpgctfllrfsseskegvtftwve 648  
Qy 626 KDISGKTQIOSVEPYTKQOLNNMSFAEIIIMGYKIKMDATNILVSPLYLYPDIPKEEAFQK 685  
Db 649 kdlsqklqigsvepytkqolnnmstaeiimgykimdattnilvsplylypdipkeeaqk 708  
Qy 686 YCRPESQEHPEADPGSAAPYLTKTKFICVTPTTCSNTIDLPMSPTLDSLMQFCNNGEGAE 745  
Db 709 ycrpesqehpeadpgsaapyltktkfivtptcsntidlpmsptlidslmqfngngegae 768  
Qy 746 PSAGGQFESLTFTDM 759  
Db 769 psaggqfestsftdm 782

RESULT 6

AAR82995

ID AAR82995 standard; Protein: 770 AA.

XX AAR82995;

XX 25-MAR-1996 (first entry)

DE Mouse liver acute phase response factor.

KW Mouse; acute phase response factor; transcription factor;  
KW interleukin-6; signal transduction; liver; antibody; antisense;  
KW ribozyme; antiinflammatory; antitumor; hypotensive; therapy.

XX Mus musculus.

XX EP676469-A2.

PD 11-OCT-1995.

PF 29-MAR-1995; 95EP-0104670.

PR 04-APR-1995; 94JP-0065825.

XX (KISH/) KISHIMOTO T.

XX Akira S, Kishimoto T;

XX WPI; 1995-346089/45.

XX N-PSDB; AAT05619.

PT New acute phase response factor - for developing inhibitory agents  
PT for treating diseases induced by cytokine(s) such as IL-6, e.g.  
XX inflammatory diseases

PS Claim 10; Page 20-22; 31pp; English.

XX The sequence represents a mouse acute phase response factor (APRF),  
CC a transcription factor related to signal transduction of  
CC interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated





transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									</
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CC The present sequence is mouse Stat3 protein fragment containing 130-358  
CC amino acids of Stat3 protein. This Stat3 fragment showed strong  
CC binding to c-Jun protein in the cell extract.  
CC The invention relates to methods for identifying interacting regions of  
CC transcription factors and methods for identifying agents which modulates  
CC the interaction between a transcription factor such as c-Jun and a Stat  
CC protein such as Stat-1 and Stat-3, useful for modulating gene  
CC transcription e.g., cellular transformation. These identifying agents are  
CC used in the treatment of dysproliferative diseases and also for treating  
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,  
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and  
CC transactivation domain.  
XX Sequence 229 AA;  
SQ  
  
Query Match 29.7%; Score 229; DB 22; Length 229;  
Best Local Similarity 100.0%; Pred. No. 8e-230;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 130 NHPTAAVYTEKQMLEQHLQDVRRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189  
DB 1 nhptaavvtekgmleqhlqdvrrvqdlqkkmkvvlenlqddfdnfyktlksqgdmqdl 60  
QY 190 GNNQSVTRQKMOQLTALDOMRRSTVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249  
DB 61 gnnqsvtrqkmqlqemltaldqmrslvselagllsameyvqkltldeeladwkrpei 120  
QY 250 ACIGGPPNICLDRLENWITSLESOLQTRQIKKLEELQOKVSYKGDPIVQHRPMLERI 309  
DB 121 acigppnicldrlenwitslesqltrqikkleelqkvsykgdplvqhrpmleri 180  
QY 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358  
DB 181 velfrnlmsafvverqpcmpmhdprrlviktgvqfttkvrlllvkfpel 229  
  
RESULT 12  
AAY72854  
ID AAY72854 standard; protein; 223 AA.  
XX  
AC AAY72854;  
XX  
DT 31-MAY-2001 (first entry)  
XX  
DE Mouse Stat3 protein fragment #12 (155-377 amino acids).  
XX  
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;  
KW cellular transformation; dysproliferative disease; cancer; psoriasis;  
KW therapy.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Region 188..204  
FT /note= "Stat3-c-Jun interaction region 2;  
FT corresponds to 342-358 position of Stat3 protein"  
XX  
XX W0200116605-A2.  
XX  
XX 08-MAR-2001.  
XX  
XX 30-AUG-2000; 2000WO-US23822.  
XX  
XX 31-AUG-1999; 99US-0387418.  
XX  
XX (UYRQ ) UNIV ROCKEFELLER.  
XX  
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;  
XX WPI; 2001-226705/23.  
XX  
XX Identifying an agent for use in modulating the interaction between

PT transcription factor c-Jun and a Stat3 protein -  
XX Claim 65; Page 79; 86pp; English.  
XX  
CC The present sequence is mouse Stat3 protein fragment containing 155-377  
CC amino acids of Stat3 protein.  
CC The invention relates to methods for identifying interacting regions of  
CC transcription factors and methods for identifying agents which modulates  
CC the interaction between a transcription factor such as c-Jun and a Stat  
CC protein such as Stat-1 and Stat-3, useful for modulating gene  
CC transcription e.g., cellular transformation. These identifying agents are  
CC used in the treatment of dysproliferative diseases and also for treating  
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,  
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and  
CC transactivation domain.  
XX Sequence 223 AA;  
SQ  
  
Query Match 29.0%; Score 223; DB 22; Length 223;  
Best Local Similarity 100.0%; Pred. No. 1.4e-223;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 155 VODLEQKMKVVENLQDDFDNFYKTLKSGQDMODLNGNNQSVTRQKMOQLTALDOMR 214  
DB 1 vqdleqkmkvvenlqddfdnfyktlksqgdmqdlngnnqsvtrqkmqlqemltaldqmr 60  
QY 215 RSIYSELAGLLSAMEYVQKTLTDEELADWKRPEIACIGGPPNICLDRLENWITSLESQ 274  
DB 61 rsiyselagllsameyvqkltldeeladwkrpelacigppnicldrlenwitslesq 120  
QY 275 LQTRQIKKLEELQOKVSYKGDPIVQHRPMLERIIVELFRNLKMSAFVVERQPCMPHDP 334  
DB 121 lqtrqikkleelqkvsykgdplvqhrpmlerivelfrnlmsafvverqpcmpmpd 180  
QY 335 RPLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377  
DB 181 rplvikgvqfttkvrlllvkfpelnyqlkikvcidkdsgdvaa 223  
  
RESULT 13  
AAR82993  
ID AAR82993 standard; protein; 770 AA.  
XX  
AC AAR82993;  
XX  
DT 25-MAR-1996 (first entry)  
XX  
DE Human placenta acute phase response factor protein.  
XX  
KW human; acute phase response factor; transcription factor;  
KW interleukin-6; signal transduction; placenta; antibody; antisense;  
KW ribozyme; antiinflammatory; antitumor; hypotensive; therapy.  
XX  
OS Homo sapiens.  
XX  
XX EP676469-A2.  
XX  
XX 11-OCT-1995.  
XX  
XX 29-MAR-1995; 95EP-0104670.  
XX  
XX 04-APR-1994; 94JP-0065825.  
XX  
XX (KISH/) KISHIMOTO T.  
XX  
XX Akira S, Kishimoto T;  
XX WPI; 1995-346089/45.  
XX N-PSDB; AAT05416.  
XX  
XX New acute phase response factor - for developing inhibitory agents  
XX for treatment of diseases induced by cytokine(s) such as IL-6, e.g.  
PT



FT /note= "Stat3-c-Jun interaction region 1;  
FT corresponds to 130-154 position of Stat3 protein"  
PN WO200116605-A2.  
PD 08-MAR-2001.  
XX  
XX 30-AUG-2000; 2000WO-US23822.  
XX 31-AUG-1999; 99US-0387418.  
XX (UYRQ ) UNIV ROCKEFELLER.  
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;  
XX WPI; 2001-226705/23..  
DR Identifying an agent for use in modulating the interaction between  
XX transcription factor c-Jun and a Stat3 protein -  
XX Claim 65; Page 77; 86pp; English.  
XX The present sequence is mouse Stat3 protein fragment containing 130-342  
XX amino acids of Stat3 protein. This Stat3 fragment showed very weak  
XX binding to c-Jun protein in the cell extract.  
XX The invention relates to methods for identifying interacting regions of  
XX transcription factors and methods for identifying agents which modulates  
XX the interaction between a transcription factor such as c-Jun and a Stat  
XX protein such as Stat-1 and Stat-3, useful for modulating gene  
XX transcription e.g., cellular transformation. These identifying agents are  
XX used in the treatment of dysproliferative diseases and also for treating  
XX cancer and psoriasis. A Stat protein comprises the N-terminal domain,  
XX coiled-coil domain, DNA binding domain, linker domain, SH2 domain and  
XX transactivation domain.  
XX Sequence 213 AA;  
Query Match 27.7%; Score 213; DB 22; Length 213;  
Best Local Similarity 100.0%; Pred. No. 3.4e-213;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 130 NHPTAAVTEKQMLEHQLQDVYKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189  
DB 1 nhptaavvtekgmleqlhqlqdvkrvqdlqkkmkvvnenlqddfdnfnyktlksqgdmqdln 60  
QY 190 GNNQSVTRKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249  
DB 61 gnnqsvtrqkmqleqmltalqdmrsvselagllsameyvvqkltldeeladwkrpei 120  
QY 250 ACIGGPPNICLDRLNWTSLAESOLOTRQOIKKLEELQKQVSKGDPVQHRPMLERI 309  
DB 121 acigppnicldrlnwnwtlsaesqltrqqlkleeiqkvskgdpvqhrpmleri 180  
QY 310 VELFRNLMSAFVVERQPCMPHDPRLVKTG 342  
DB 181 velfrnlmsafvverqpcmpmhdprrlviktg 213  
RESULT 16  
ID AAY72862  
XX AAY72862 standard; protein: 229 AA.  
AC AAY72862;  
XX  
DT 31-MAY-2001 (first entry)  
XX  
DE Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).  
XX  
KW Mouse; Stat3 protein; transcription factor: c-Jun; gene transcription;  
KW cellular transformation; dysproliferative disease; cancer; psoriasis;  
KW therapy; mutant; mutein.  
XX

OS Mus musculus.  
XX Key Location/Qualifiers  
FH Region 1..25  
FT /note= "Stat3-c-Jun interaction region 1;  
FT corresponds to 130-154 position of Stat3 protein"  
FT Misc-difference 19  
FT /note= "Wild type Leu substituted with Ala;  
FT corresponds to 148 position of Stat-3 protein"  
FT 213..229  
FT /note= "Stat3-c-Jun interaction region 2;  
FT corresponds to 342-358 position of Stat3 protein"  
XX  
XX WO200116605-A2.  
XX 08-MAR-2001.  
XX 30-AUG-2000; 2000WO-US23822.  
XX 31-AUG-1999; 99US-0387418.  
XX (UYRQ ) UNIV ROCKEFELLER.  
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;  
XX WPI; 2001-226705/23.  
XX Identifying an agent for use in modulating the interaction between  
XX transcription factor c-Jun and a Stat3 protein -  
XX Claim 66; Page 85; 86pp; English.  
XX The present sequence is mouse Stat3 mutant (L148A) protein fragment  
XX containing 130-358 amino acids of Stat3 protein. This mutant is obtained  
XX by replacing Leu 148 with Ala in Stat3 protein.  
XX The invention relates to methods for identifying interacting regions of  
XX transcription factors and methods for identifying agents which modulates  
XX the interaction between a transcription factor such as c-Jun and a Stat  
XX protein such as Stat-1 and Stat-3, useful for modulating gene  
XX transcription e.g., cellular transformation. These identifying agents are  
XX used in the treatment of dysproliferative diseases and also for treating  
XX cancer and psoriasis. A Stat protein comprises the N-terminal domain,  
XX coiled-coil domain, DNA binding domain, linker domain, SH2 domain and  
XX transactivation domain.  
XX Sequence 229 AA;  
Query Match 27.3%; Score 210; DB 22; Length 229;  
Best Local Similarity 100.0%; Pred. No. 4.9e-210;  
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 149 QDVPRKRVQDLEOKMKVVENLQDDFDNFYKTLKSGQDMQDLNNGNSVTROKMOOLEQMLT 208  
DB 20 qdvprkrvqdlqkkmkvvnenlqddfdnfnyktlksqgdmqdlngnqsvtrqkmqleqmlt 79  
QY 209 ALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEIACIGGPPNICLDRLNWT 268  
DB 80 alqdmrsvselagllsameyvvqkltldeeladwkrpeiaccigppnicldrlnwt 139  
QY 269 SLAESQLOTRQOIKKLEELQKQVSKGDPVQHRPMLERIIVELFRNLMSAFVVERQPC 328  
DB 140 slaesqltrqqlkleeiqkvskgdpvqhrpmleriivelfrnlmsafvverqpc 199  
QY 329 MPMPHDPRLVKTGVOFTTKVRLLVKRPPEL 358  
DB 200 mpmhdprrlviktgvqfttkvrlvvkfpel 229  
RESULT 17  
ID AAY72861  
XX AAY72861 standard; protein: 228 AA.  
XX



```

Query Match      26.9%; Score 207; DB 22; Length 229;
Best Local Similarity 100.0%; Pred. No. 6.5e-207;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 RKRVDLEQKMKVVENLQDDFDNFYKTLKSGDMDLNGNQSIVTRQKMQQLEQMLTALD 211
      |||
Db 23 rkrvqdeqkmkvvlenlqddfdfnfnyktlksqgdmqdlngnqsvtrqkmgqleqmltald 82
      |||
QY 212 QMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEIACIGGPPNICLDRLNNWITSIA 271
      |||
Db 83 qmrirsivselagllsameyvqkltldeeadwkrpeiacigppnicldrlenwitsia 142
      |||
QY 272 ESQLOTROQIKKLEELQOKVSKYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPM 331
      |||
Db 143 esqltrqrqikkleelqokvskygdpivqhrpmlerivelfrlnlmksafvverqpcmpm 202
      |||
QY 332 HPDRPLVKTGVQFTTKVRLLLVKFPEL 358
      |||
Db 203 hpdprlviktgvqfttkvrlllvkfpel 229

RESULT 19
AAY72860
ID AAY72860 standard; protein; 229 AA.
XX
AC AAY72860;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 mutant (L148A,V151A,T346A,K348A,R350A) protein fragment.
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy; mutant; muten.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FH Region 1..25
FT /note= "Stat3-c-Jun interaction region 1;
FT corresponds to 130-154 position of Stat3 protein"
FT Misc-difference 19
FT /note= "Wild type Leu substituted with Ala;
FT corresponds to 148 position of Stat-3 protein"
FT Misc-difference 22
FT /note= "Wild type Val substituted with Ala
FT corresponds to 151 position of Stat-3 protein"
FT Region 213..229
FT /note= "Stat3-c-Jun interaction region 2;
FT corresponds to 342-358 position of Stat3 protein"
FT Misc-difference 217
FT /note= "Wild type Thr substituted with Ala
FT corresponds to 346 position of Stat-3 protein"
FT Misc-difference 219
FT /note= "Wild type Lys substituted with Ala
FT corresponds to 348 position of Stat-3 protein"
FT Misc-difference 221
FT /note= "Wild type Arg substituted with Ala
FT corresponds to 350 position of Stat-3 protein"
XX
XX WO200116605-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 30-AUG-2000; 2000WO-US23822.
XX
XX PR 31-AUG-1999; 99US-0387418.
XX
XX PA (UYRQ ) UNIV ROCKEFELLER.
XX
XX PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
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XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein .
XX
XX Example 4; Page -: 86pp; English.
XX
XX The present sequence is mouse Stat3 mutant protein fragment containing
XX 130-358 amino acids of Stat3 protein. This mutant is obtained by
XX replacing Leu 148 with Ala, Val 151 with Ala, Thr 346 with Ala, Lys 348
XX with Ala and Arg 350 with Ala in the Stat3 protein.
XX The invention relates to methods for identifying interacting regions of
XX transcription factors and methods for identifying agents which modulates
XX the interaction between a transcription factor such as c-Jun and a Stat
XX protein such as Stat-1 and Stat-3, useful for modulating gene
XX transcription e.g., cellular transformation. These identifying agents are
XX used in the treatment of dysproliferative diseases and also for treating
XX cancer and psoriasis. A Stat protein comprises the N-terminal domain,
XX coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
XX transactivation domain.
XX
XX Sequence 229 AA:

Query Match      25.2%; Score 194; DB 22; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 RKRVDLEQKMKVVENLQDDFDNFYKTLKSGDMDLNGNQSIVTRQKMQQLEQMLTALD 211
      |||
Db 23 rkrvqdeqkmkvvlenlqddfdfnfnyktlksqgdmqdlngnqsvtrqkmgqleqmltald 82
      |||
QY 212 QMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEIACIGGPPNICLDRLNNWITSIA 271
      |||
Db 83 qmrirsivselagllsameyvqkltldeeadwkrpeiacigppnicldrlenwitsia 142
      |||
QY 272 ESQLOTROQIKKLEELQOKVSKYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPM 331
      |||
Db 143 esqltrqrqikkleelqokvskygdpivqhrpmlerivelfrlnlmksafvverqpcmpm 202
      |||
QY 332 HPDRPLVKTGVQF 345
      |||
Db 203 hpdprlviktgvqf 216

RESULT 20
AAY72855
ID AAY72855 standard; protein; 185 AA.
XX
AC AAY72855;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #13 (193-377 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
XX OS Mus musculus.
XX
XX FH Key Location/Qualifiers
XX FH Region 150..166
XX /note= "Stat3-c-Jun interaction region 2;
XX corresponds to 342-358 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 30-AUG-2000; 2000WO-US23822.
XX
```

```
PR 31-AUG-1999; 99US-0387418.
XX (UYRQ ) UNIV ROCKEFELLER.
PA Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
PI WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein -
XX
XX Claim 65; Page 80; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 193-377
XX amino acids of Stat3 protein.
XX The invention relates to methods for identifying interacting regions of
XX transcription factors and methods for identifying agents which modulates
XX the interaction between a transcription factor such as c-Jun and a Stat
XX protein such as Stat-1 and Stat-3, useful for modulating gene
XX transcription e.g., cellular transformation. These identifying agents are
XX used in the treatment of dysproliferative diseases and also for treating
XX cancer and psoriasis. A Stat protein comprises the N-terminal domain,
XX coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
XX transactivation domain.
XX Sequence 185 AA;
SQ
Query Match 24.0%; Score 185; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.4e-184;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 193 QSVTRQKMOOLEQMLTALDOMRRSIVSELAGLSAMEYVQKTLTDEELADWKRPEIACI 252
DB 1 qsvtrqkmqlqeqmltaldqmrirsivselagllsameyvqktltdeeladwkrpeiaci 60
QY 253 GPPNCLDRLENNWITSLAESQLOTRQOIKKLEELQOKVSKGDPVQHRPMLERIVEL 312
DB 61 gppncldrleennwitslaesqltrqoikkleelqokvskgdpvqhrpmlerivel 120
QY 313 FRNLKMSAFVVERQPCMPHDPRLVITKGVQFTTKVRLLVKFPPELNYQLIKVCIDKDS 372
DB 121 frnlkmsafvverqpcmpdpvrlviktgvqfttkvrlvlkvfpelnyqlikvcidkds 180
QY 373 GDVAA 377
DB 181 gdvaa 185
RESULT 21
AAY72848
ID AAY72848 standard; protein; 176 AA.
XX
XX AAY72848;
XX
XX 31-MAY-2001 (first entry)
XX
XX Mouse Stat3 protein fragment #6 (107-282 amino acids).
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX cellular transformation; dysproliferative disease; cancer; psoriasis;
XX therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Key 24...48
XX Region /note= "Stat3-c-Jun interaction region 1;
XX corresponds to 130-154 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
PD
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XX 30-AUG-2000; 2000WO-US23822.
XX
XX 31-AUG-1999; 99US-0387418.
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein -
XX
XX Claim 65; Page 74-75; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 107-282
XX amino acids of Stat3 protein.
XX The invention relates to methods for identifying interacting regions of
XX transcription factors and methods for identifying agents which modulates
XX the interaction between a transcription factor such as c-Jun and a Stat
XX protein such as Stat-1 and Stat-3, useful for modulating gene
XX transcription e.g., cellular transformation. These identifying agents are
XX used in the treatment of dysproliferative diseases and also for treating
XX cancer and psoriasis. A Stat protein comprises the N-terminal domain,
XX coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
XX transactivation domain.
XX Sequence 176 AA;
SQ
Query Match 22.9%; Score 176; DB 22; Length 176;
Best Local Similarity 100.0%; Pred. No. 9.9e-175;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 107 RCLWERSRLQTAATAAQGGQANHPTRAHVTEKQOMLEQHLQDVKRVRQDLQKMKVVE 166
DB 1 rclweersrllqtaataaqqggqanhptraavvtekqqlqdvkrvrqdlqkmkvve 60
QY 167 NLQDDFFV NYKTLKSGQDMQDLNGNQSVTROKMOOLEQMLTALDOMRRSIVSELAGLILS 226
DB 61 nlqddfdvnyktlksqgdmqdlngnqsvtrqkmgqlemltaldmrrsivselagilis 120
QY 227 AMEYVQKTLTDEELADWKRPEIACIGGPPNICLDRLNWIITSLAESQLOTRQOIK 282
DB 121 ameyvqktltdeeladwkrpeiacigppnicldrlenwitslaesqltrqqik 176
RESULT 22
AAY72840
ID AAY72840 standard; protein; 154 AA.
XX
XX AAY72840;
XX
XX 31-MAY-2001 (first entry)
XX
XX Mouse Stat3 protein fragment #1 (1-154 amino acids).
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX cellular transformation; dysproliferative disease; cancer; psoriasis;
XX therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Key 1..130
XX Domain /note= "N-terminal domain"
XX Region 130..154
XX FT /note= "Stat3-c-Jun interaction region 1"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
PD
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XX 30-AUG-2000; 2000WO-US23822.
PF
XX
XX 31-AUG-1999; 99US-0387418.
PR
XX
XX (UYRQ ) UNIV ROCKEFELLER.
PA
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
PI
XX
XX WPI; 2001-226705/23.
DR
XX
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein -
PT
XX
XX Claim 65; Page 75-76; 86pp; English.
PS
XX
XX The present sequence is mouse Stat3 protein fragment containing 107-249
CC amino acids of Stat3 protein.
CC The invention relates to methods for identifying interacting regions of
CC transcription factors and methods for identifying agents which modulates
CC the interaction between a transcription factor such as c-Jun and a Stat
CC protein such as Stat-1 and Stat-3, useful for modulating gene
CC transcription e.g., cellular transformation. These identifying agents are
CC used in the treatment of dysproliferative diseases and also for treating
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
CC transactivation domain.
CC
XX Sequence 143 AA;
SQ
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XX 30-AUG-2000; 2000WO-US23822.
PF
XX
XX 31-AUG-1999; 99US-0387418.
PR
XX
XX (UYRQ ) UNIV ROCKEFELLER.
PA
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
PI
XX
XX WPI; 2001-226705/23.
DR
XX
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein -
PT
XX
XX Claim 65; Page 66-67; 86pp; English.
PS
XX
XX The present sequence is mouse Stat3 protein fragment containing 1-154
CC amino acids of Stat3 protein. This Stat3 fragment showed very weak
CC binding to c-Jun protein in the cell extract.
CC The invention relates to methods for identifying interacting regions of
CC transcription factors and methods for identifying agents which modulates
CC the interaction between a transcription factor such as c-Jun and a Stat
CC protein such as Stat-1 and Stat-3, useful for modulating gene
CC transcription e.g., cellular transformation. These identifying agents are
CC used in the treatment of dysproliferative diseases and also for treating
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
CC transactivation domain.
CC
XX Sequence 154 AA;
SQ
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```
Query Match 18.6%; Score 143; DB 22; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.9e-140;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 RCLWEESRLQLTAATAAQGGQGANHPTAAVTEKQOMLEQHLQDYVRKRQDLQKMKVVE 166
Db 1 rclweesrlqltaataaqggqganhptaavtekgmleqlhldvkrvqdlqkmkvve 60

QY 167 NLQDDFDNFYKTKSGQMDLNGNNSVTROKMOOLEQMLTALDOMRRSIVSELAGLLS 226
Db 61 nlqddfdnfyktksgqmdlngnnsvtrokmqleqmltalqdmrrsivselaglls 120

QY 227 AMEYVOKTLTDEELADWKRPEI 249
Db 121 ameyvoktldeeladwkrpei 143

RESULT 24
AAY07240
ID AAY07240 standard; protein; 141 AA.
XX
XX AAY07240;
XX
XX 06-JUL-1999 (first entry)
XX
XX Fragment of human hepatic STAT3 protein.
XX
XX Placenta; isoform; human; STAT3; intracellular; transcription factor;
KW Signal Transducer and Activator of Transcription; allele; growth arrest;
KW hepatic acute-phase protein; monocytic cell; myeloma; autoimmune disease;
KW inflammation.
XX
XX Homo sapiens.
XX
XX EP906953-A1.
XX
XX 07-APR-1999.
XX
XX 16-SEP-1997; 97EP-0116061.
XX
XX 16-SEP-1997; 97EP-0116061.
XX
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```
Query Match 20.0%; Score 154; DB 22; Length 154;
Best Local Similarity 100.0%; Pred. No. 7.2e-152;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLQKHLYSDTFPMELRQFLAPWIESODWAYAASKESHATLVFHNH 60
Db 1 maqwnlqqldtrylkqlhlysdtfpmeqrflapwiesqdwyaaskeshatlvfhn 60

QY 61 LGEIDQOYSRFLQESNVLYQHNRRIKQFLQSRYLKPKMEIARIVARCLWEESRLQATA 120
Db 61 lgeidqysrflqesnvlyqhnrrikqflqsrylekpkmeiarivarclweesrlqata 120

QY 121 TAAQGGQGANHPTAAVTEKQOMLEQHLQDYVRKR 154
Db 121 taaggqganhptaavtekgmleqlhldvkrkr 154

RESULT 23
AAY72849
ID AAY72849 standard; protein; 143 AA.
XX
XX AAY72849;
XX
XX 31-MAY-2001 (first entry)
XX
XX Mouse Stat3 protein fragment #7 (107-249 amino acids).
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH 24..48
FT Region /note= "Stat3-c-Jun interaction region 1;
FT corresponds to 130-154 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
```

PA	(ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.	
XX	Della Pietra L, Serlupi-Crescenzi O;	
XX	WP1; 1999-207107/18.	
DR	N-PSDB; AAX29976.	
XX	New allelic variant of human STAT3 useful in treating autoimmune or	
PT	inflammatory diseases	
PT	Claim 2; Page 10-11; 22pp; English.	
XX	This sequence represents a fragment of the hepatic allelic isoform	
XX	of human Signal Transducer and Activator of Transcription (STAT3)	
CC	intracellular transcription factor (Akira et al., Cell 77, 63-71	
CC	(1994)). The invention relates to isolation of allelic variants of	
CC	the placental hSTAT3 sequence. hSTAT3 plays a role in the upregulation	
CC	of hepatic acute-phase proteins, growth arrest of monocytic cells and	
CC	in the survival of myeloma cells and so may be used to treat or diagnose	
CC	autoimmune or inflammatory diseases.	
XX	Sequence 141 AA;	
SO		
Query Match 18.3%; Score 141; DB 20; Length 141;		
Best Local Similarity 100.0%; Pred. No. 2.3e-138;		
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	564 WLDNIIDLKYLALWNEGYIMGFISKERERATLTKPPGTFLLRFSSESKGGVTFTW 623	
Db	1 wldnidlkvkylalwnegyimgfiskereraistkppgtflrrfseskeggvtftw 60	
QY	624 VEKDISGKTQIOSVEPYTKQOLNNMSPAEIIMGYKIMDATNILVSPILVLYPDIPKEEAF 683	
Db	61 vekdisgktqigsvepytkqolnnmsfaeiimgykimdatnilvspilvlypdipkeef 120	
QY	684 GKYCRPESQEHPEADPGSAAP 704	
Db	121 gkycrpesqehpeadpgsaap 141	
RESULT 25		
AAB19973	AAB19973 standard; Protein; 173 AA.	
XX	AC	AAB19973;
XX	DT	28-MAR-2001 (first entry)
XX	DE	Human STAT-3 DNA binding domain.
XX	KW	STAT-3; signal transducer and activator of transcription 3;
XX	KW	human; crystal; drug screening; DNA binding domain.
XX	OS	Homo sapiens.
XX	PN	US6160092-A.
XX	PD	12-DEC-2000.
XX	PF	29-MAY-1998; 98US-0087465.
XX	PR	29-MAY-1998; 98US-0087465.
XX	PA	(UYRQ ) UNIV ROCKEFELLER.
XX	PI	Chen X, Darnell JE, Kuriyan J, Vinkemeier U, Zhao Y, Jeruzalmi D;
XX	DR	WP1; 2001-101568/11.
XX	DR	N-PSDB; AAX89239.
XX	PT	Novel crystal useful in drug screening assays, comprises portion of
XX	PT	signal transducer, activator of transcription and duplex DNA

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XX	Claim 8; Column 99-102; 206pp; English.	
PS	The present sequence is that of the DNA binding domain of human	
XX	signal transducer and activator of transcription 3 (STAT-3), i.e.	
CC	amino acids 321-493 of the full-length protein (see AAB19964). The	
CC	domain includes an immunoglobulin-type fold. The invention provides	
CC	a crystal of a core portion of a STAT protein in dimer form with an	
CC	18-mer duplex DNA (see AAX89233) that contains a binding site for	
CC	the STAT dimer. The core portion comprises a coiled-coil domain,	
CC	the DNA binding domain, a SH2 domain and a linker domain that joins	
CC	the DNA binding and SH2 domains. The crystal is of sufficient	
CC	quality to perform X-ray crystallography studies. Methods of	
CC	preparing the crystals are included in the invention. Knowledge of	
CC	the STAT protein's 3-dimensional structure will aid in	
CC	structure-based drug design. The crystal can be used in drug	
CC	screening assays to identify agonist and antagonist compounds.	
CC	Antagonists can be used to treat inflammation, allergy, asthma and	
CC	leukaemia, and agonists to treat anaemia, neutropenia,	
CC	thrombocytopenia, cancer, obesity, viral diseases, growth	
CC	retardation, and other conditions characterized by insufficient	
CC	STAT activity. Fusion proteins comprising a portion of STAT,	
CC	especially the DNA binding domain, and a fusion partner are also	
CC	disclosed.	
XX	Sequence 173 AA;	
SO		
Query Match 18.1%; Score 139; DB 22; Length 173;		
Best Local Similarity 100.0%; Pred. No. 3.3e-136;		
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	321 FVVEROPCPMPHPDRPLVIKTVQFTTKYRLLVKTPPELVYQLKIKVCIDKSDVAALRG 380	
Db	1 fvverqpcmpmpdrplviktgvfttkvrlivktpelnyqlkikvcidkdsqdvaaalrg 60	
QY	381 SRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCNGGRANCASLIIVTEELHLIT 440	
Db	61 srkfnilgtntkvmnmeesngslsaefkhltlreqrcnggrancdasliivteelhlit 120	
QY	441 FETEVYHQGLKIDLETHSL 459	
Db	121 fetevyhqqikidlethsl 139	
RESULT 26		
AAY07241	AAY07241 standard; Protein; 141 AA.	
XX	AC	AAY07241;
XX	DT	06-JUL-1999 (first entry)
XX	DE	Fragment of mouse hepatic STAT3 protein.
XX	KW	Placenta; isoform; human; STAT3; intracellular; transcription factor;
XX	KW	Signal Transducer and Activator of Transcription; allele; growth arrest;
XX	KW	hepatic acute-phase protein; monocytic cell; myeloma; autoimmune disease;
XX	OS	inflammation.
XX	PN	Mus sp.
XX	PN	EP906953-Al.
XX	PD	07-APR-1999.
XX	PF	16-SEP-1997; 97EP-0116061.
XX	PR	16-SEP-1997; 97EP-0116061.
XX	PA	(ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX	PI	Della Pietra L, Serlupi-Crescenzi O;



XX WPI; 1999-207107/18.  
DR N-PSDB; AAX29977.  
XX  
XX New allelic variant of human STAT3 useful in treating autoimmune or  
PT inflammatory diseases  
PS  
XX  
XX Disclosure; Page 12-13; 22pp; English.  
PS  
XX  
XX This sequence represents a fragment of the hepatic allelic isoform  
CC of mouse Signal Transducer and Activator of Transcription (STAT3)  
CC intracellular transcription factor (Akira et al., Cell 77, 63-71  
CC (1994)). The invention relates to isolation of allelic variants of  
CC the placental human STAT3 sequence. hSTAT3 plays a role in the  
CC upregulation of hepatic acute-phase proteins, growth arrest of monocytic  
CC cells and in the survival of myeloma cells and so may be used to treat  
CC or diagnose autoimmune or inflammatory diseases.  
XX  
SQ Sequence 141 AA;  
  
Query Match 17.9%; Score 138; DB 20; Length 141;  
Best Local Similarity 100.0%; Pred. No. 3.1e-135; Length 141;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 564 WLDNIIDLVKYIILALWNEGYIMGFISKERERAILSTKPGTFLLRFSSESKGGVTFW 623  
Db 1 wldniidlvkkyialwnegyimgfiskerailstckpgtflrrfsesskeggvtfw 60  
  
Qy 624 VEKDISGKTQIQSVPTKQOLNMSFAEIIIMGYKINDATNIIIVSLVLYLPDIPKEAF 683  
Db 61 vekdisgktqiqsvptkqolnmsfaeiiimgykindatniiivslvlylpdipkeaf 120  
  
Qy 684 GKCRPESQEHPEADPGS 701  
Db 121 gkcrpesqehpeadpgs 138  
  
RESULT 27  
AAY72856  
ID AAY72856 standard; protein; 129 AA.  
XX  
AC AAY72856;  
XX  
DT 31-MAY-2001 (first entry)  
XX  
DE Mouse Stat3 protein fragment #14 (249-377 amino acids).  
XX  
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;  
KW cellular transformation; dysproliferative disease; cancer; psoriasis;  
KW therapy.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Region 94..110  
FT /note= "Stat3-c-Jun interaction region 2;  
FT corresponds to 342-358 position of Stat3 protein"  
XX  
PN WO200116605-A2.  
XX  
XX 08-MAR-2001.  
XX  
XX 30-AUG-2000; 2000WO-US23822.  
XX  
XX 31-AUG-1999; 99US-0387418.  
XX  
XX (UYRQ ) UNIV ROCKEFELLER.  
XX  
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;  
XX WPI; 2001-226705/23.  
XX

PT Identifying an agent for use in modulating the interaction between  
PT transcription factor c-Jun and a Stat3 protein -  
XX  
XX Claim 65; Page 80-81; 86pp; English.  
XX  
XX The present sequence is mouse Stat3 protein fragment containing 249-377  
CC amino acids of Stat3 protein.  
CC The invention relates to methods for identifying interacting regions of  
CC transcription factors and methods for identifying agents which modulates  
CC the interaction between a transcription factor such as c-Jun and a Stat  
CC protein such as Stat-1 and Stat-3, useful for modulating gene  
CC transcription e.g., cellular transformation. These identifying agents are  
CC used in the treatment of dysproliferative diseases and also for treating  
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,  
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and  
CC transactivation domain.  
XX  
SQ Sequence 129 AA;  
  
Query Match 16.8%; Score 129; DB 22; Length 129;  
Best Local Similarity 100.0%; Pred. No. 6.7e-126;  
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 249 IACIGPPNICLDRLNWTSLAESQLTROQIKKLEELQOKVSKGDPVOHRPMLER 308  
Db 1 iacigppnicldrlenwtslaesqltrqqikkleelqkvskgdpvqhrpmler 60  
  
Qy 309 IVELFNLMKSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLILVKFPELNYQIKIKVC 368  
Db 61 ivelfnmlksafvverqpcmpmhdprrlvktgvqfttkvrlilvkfpelnqyqkikvc 120  
  
Qy 369 DKDSGDVAA 377  
Db 121 dkdsgdvaa 129  
  
RESULT 28  
AAY72852  
ID AAY72852 standard; protein; 128 AA.  
XX  
AC AAY72852;  
XX  
DT 31-MAY-2001 (first entry)  
XX  
DE Mouse Stat3 protein fragment #10 (155-282 amino acids).  
XX  
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;  
KW cellular transformation; dysproliferative disease; cancer; psoriasis;  
KW therapy.  
XX  
OS Mus musculus.  
XX  
XX WO200116605-A2.  
XX  
XX 08-MAR-2001.  
XX  
XX 30-AUG-2000; 2000WO-US23822.  
XX  
XX 31-AUG-1999; 99US-0387418.  
XX  
XX (UYRQ ) UNIV ROCKEFELLER.  
XX  
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;  
XX WPI; 2001-226705/23.  
XX  
XX Identifying an agent for use in modulating the interaction between  
PT transcription factor c-Jun and a Stat3 protein -  
XX  
XX Claim 65; Page 78; 86pp; English.  
XX  
XX The present sequence is mouse Stat3 protein fragment containing 155-282

CC amino acids of Stat3 protein.  
CC The invention relates to methods for identifying interacting regions of  
CC transcription factors and methods for identifying agents which modulates  
CC the interaction between a transcription factor such as c-Jun and a Stat  
CC protein such as Stat-1 and Stat-3, useful for modulating gene  
CC transcription e.g., cellular transformation. These identifying agents are  
CC used in the treatment of dysproliferative diseases and also for treating  
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,  
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and  
CC transactivation domain.  
XX  
SQ Sequence 128 AA;  
  
Query Match 16.6%; Score 128; DB 22; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.3e-125; Indels 0; Gaps 0;  
Matches 128; Conservative 0; Mismatches 0;  
  
QY 155 VQDLQKMKVVENLQDDFDNFYKTLKSQGMODLNGNOSVTRQKMQOLEQMLTALDQMR 214  
Db 1 vqdlqkmkvvenlqddfdnfykltksgqdmqdlngnqsvtrqknqgleqmltaldqmr 60  
  
QY 215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEIACIGCPPNICLDRLNWTSLAESQ 274  
Db 61 rsiivselagllsameyvqkltldeeladwkrpeiacigcppnicldrlenwitslaesq 120  
  
QY 275 LQTRQQIK 282  
Db 121 lqtrqqik 128  
  
RESULT 29  
AAW03167  
ID AAW03167 standard; Protein: 112 AA.  
XX  
AC AAW03167;  
XX  
DT 24-OCT-1996 (first entry)  
XX  
DE Mouse STAT4 DNA binding domain.  
XX  
KW STAT; STAT4; DNA binding domain;  
KW signal transducer and activator of transcription; ligand; receptor;  
KW oncogenesis; inflammation; autoimmune disease; antagonist; therapy.  
XX  
OS Mus sp.  
XX  
PN W09620954-A2.  
XX  
PD 11-JUL-1996.  
XX  
PF 28-DEC-1995; 95WO-US17025.  
XX  
PR 06-JAN-1995; 95US-0369796.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Darnell JE, Horvath CM, Wen Z, Zhong Z;  
XX  
DR WPI; 1996-333941/33.  
XX  
PT New STAT protein DNA-binding domain peptide(s) - useful for  
PT diagnosing, preventing or treating cellular dysfunction, e.g.  
PT oncogenesis, inflammation, parasitic disease or autoimmunity  
XX  
PS Claim 3; Page 110; 138pp; English.  
XX  
CC DNA binding domains (AAW03165, AAW03167, AAW03169, AAW03171, AAW03173  
CC and AAW03175) of signal transducer and activator of transcription  
CC (STAT) proteins are capable of both receptor recognition and  
CC message delivery via DNA binding in a receptor-ligand specific  
CC manner. They directly participate in the interaction with the  
CC ligand-bound receptor at the cell surface and in the activity of

CC transcription in the nucleus as DNA binding proteins. The  
CC DNA binding domain given in AAW03167 is found in mouse STAT4  
CC (see also AAW03176). It was defined by exchanging regions between  
CC 2 STAT proteins and assaying for DNA site binding preference. It  
CC can be used to screen for antagonists that inhibit STAT-mediated  
CC signal transduction and activation of transcription, and to raise  
CC antibodies.  
XX  
SQ Sequence 112 AA;  
  
Query Match 14.5%; Score 112; DB 17; Length 112;  
Best Local Similarity 100.0%; Pred. No. 3e-108;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 403 SLSAEFKHLTLREQRCGNGRANCDAASLIVTEELHLITFETEVYHQLKIDLETHSLPVP 462  
Db 1 slsaefkhltlreqrcgnggrancdaslvtelhlitfetevyhqlkidlthslpvp 60  
  
QY 463 VISNICQMPNAWASILWYNMLTNPNKNVFFTKPPIGTMDQVAEVLWQFSS 514  
Db 61 visnicqmpnawasilwynmltnpnknvfftkppigtmdqvaevlswqfss 112  
  
RESULT 30  
AAY07239  
ID AAY07239 standard; Protein: 141 AA.  
XX  
AC AAY07239;  
XX  
DT 06-JUL-1999 (first entry)  
XX  
DE Fragment of human placental STAT3 protein.  
XX  
KW Placenta; isoform; human; STAT3; intracellular; transcription factor;  
KW Signal Transducer and Activator of Transcription; allele; growth arrest;  
KW hepatic acute-phase protein; monocytic cell; myeloma; autoimmune disease;  
KW inflammation.  
XX  
OS Homo sapiens.  
XX  
PN EP906953-A1.  
XX  
PD 07-APR-1999.  
XX  
PF 16-SEP-1997; 97EP-0116061.  
XX  
PR 16-SEP-1997; 97EP-0116061.  
XX  
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
XX  
PI Della Pietra L, Serlupi-Crescenzi O;  
XX  
DR WPI; 1999-207107/18.  
DR N-PSDB; AAX29975.  
XX  
XX New allelic variant of human STAT3 useful in treating autoimmune or  
XX inflammatory diseases  
XX  
PS Disclosure; Page 8-9; 22pp; English.  
XX  
CC This sequence represents a fragment of the placental isoform of human  
CC Signal Transducer and Activator of Transcription (STAT3) intracellular  
CC transcription factor (Akira et al., Cell 77, 63-71 (1994)). The  
CC invention relates to isolation of allelic variants of the placental  
CC hSTAT3 sequence. hSTAT3 plays a role in the upregulation of hepatic  
CC acute-phase proteins, growth arrest of monocytic cells and in the  
CC survival of myeloma cells and so may be used to treat or diagnose  
CC autoimmune or inflammatory diseases.  
XX  
SQ Sequence 141 AA;

Query Match 13.4%; Score 103; DB 20; Length 141;  
Best Local Similarity 100.0%; Pred. No. 8.7e-99; Indels 0; Gaps 0;  
Matches 103; Conservative 0; Mismatches 0;

QY 564 WLDNTIDLVKKYILALWNEGVIKGERERAILSTKPPGTFLLRFSSESKEGGVTFTW 623  
DB 1 WLDNTIDLVKKYILALWNEGVIKGERERAILSTKPPGTFLLRFSSESKEGGVTFTW 60

QY 624 VEKDISGKTQIOSVEPYTKQOLNNMSPAEIIMGYKIMDATNIL 666  
DB 61 vekdisgktqigsvepytkqqlnnmsfaeiimgykimdattail 103

RESULT 31  
ID AAY72857  
XX AAY72857 standard; protein: 96 AA.  
AC AAY72857;  
DT 31-MAY-2001 (first entry)  
XX Mouse Stat3 protein fragment #15 (282-377 amino acids).  
DE Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;  
KW cellular transformation; dysproliferative disease; cancer; psoriasis;  
KW therapy.  
XX Mus musculus.  
OS  
FH Key Location/Qualifiers  
FT Region 61..77  
FT /note= "Stat3-c-Jun interaction region 2;  
FT corresponds to 342-358 position of Stat3 protein"  
XX  
PN W0200116605-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US23822.  
XX  
PR 31-AUG-1999; 99US-0387418.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;  
XX WPI; 2001-226705/23.  
XX  
PT Identifying an agent for use in modulating the interaction between  
PT transcription factor c-Jun and a Stat3 protein -  
XX  
PS Claim 65; Page 81; 86pp; English.  
XX  
CC The present sequence is mouse Stat3 protein fragment containing 282-377  
CC amino acids of Stat3 protein.  
CC The invention relates to methods for identifying interacting regions of  
CC the interaction between a transcription factor such as c-Jun and a Stat  
CC protein such as Stat-1 and Stat-3, useful for modulating gene  
CC transcription e.g., cellular transformation. These identifying agents are  
CC used in the treatment of dysproliferative diseases and also for treating  
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,  
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and  
CC transactivation domain.  
XX  
SQ Sequence 96 AA:

Query Match 12.5%; Score 96; DB 22; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.2e-91;  
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 KLEELQKQVSKGDPITVQHRPMLEERIVELFNLMKSAFVVERQPCMPMPHDPRLVIKT 341

DB 1 KLEELQKQVSKGDPITVQHRPMLEERIVELFNLMKSAFVVERQPCMPMPHDPRLVIKT 60

QY 342 GVQFTTKVRLLVKFPPELNLVKLIKVCIDKDSGDVAA 377

DB 61 gvqfttkvrllvkfpelnyqkikvcidkdsgdvaa 96

RESULT 32  
ID AAY72853  
XX AAY72853 standard; protein: 95 AA.  
AC AAY72853;  
DT 31-MAY-2001 (first entry)  
XX Mouse Stat3 protein fragment #11 (155-249 amino acids).  
DE Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;  
KW cellular transformation; dysproliferative disease; cancer; psoriasis;  
KW therapy.  
XX Mus musculus.  
OS  
FH Key Location/Qualifiers  
FT Region 155..249  
FT /note= "Stat3-c-Jun interaction region 2;  
FT corresponds to 342-358 position of Stat3 protein"  
XX  
PN W0200116605-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US23822.  
XX  
PR 31-AUG-1999; 99US-0387418.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;  
XX WPI; 2001-226705/23.  
XX  
PT Identifying an agent for use in modulating the interaction between  
PT transcription factor c-Jun and a Stat3 protein -  
XX  
PS Claim 65; Page 78; 86pp; English.  
XX  
CC The present sequence is mouse Stat3 protein fragment containing 155-249  
CC amino acids of Stat3 protein.  
CC The invention relates to methods for identifying interacting regions of  
CC the interaction between a transcription factor such as c-Jun and a Stat  
CC protein such as Stat-1 and Stat-3, useful for modulating gene  
CC transcription e.g., cellular transformation. These identifying agents are  
CC used in the treatment of dysproliferative diseases and also for treating  
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,  
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and  
CC transactivation domain.  
XX  
SQ Sequence 95 AA:

Query Match 12.3%; Score 95; DB 22; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1.3e-90;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 VQDLQKMKVVENLQDDFDENYKTLKSGODMLNGNQSVTROKMOLEQMLTALDQMR 214  
DB 1 vqdleqkmkvvenlqddfdfnkylksqgdmgdngnqsvtrqkmqleqmltaldqmr 60

QY 215 RSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI 249  
DB 61 rsivselagllsameyvgkltldeeladwkrpei 95

Search completed: March 20, 2002, 08:46:10

us-08-212-185-12.olig.rag

Wed Mar 20 11:17:36 2002

Job time: 242 sec



GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: March 20, 2002, 08:42:28 ; Search time 64.76 Seconds  
(without alignments)  
267.565 Million cell updates/sec

Title: US-08-212-185-12  
Perfect score: 770  
Sequence: 1 MAOWNQLQDLTRYLKOLHQ.....QFESLTFMDLTSECATSPM 770

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	100.0	770	1	US-08-369-796-12
2	770	100.0	770	2	US-08-852-091-12
3	770	100.0	770	2	US-08-820-754-12
4	770	100.0	770	3	US-08-956-652-12
5	770	100.0	770	3	US-08-956-869-12
6	770	100.0	770	4	US-08-948-547-12
7	770	100.0	770	4	US-09-364-970-3
8	770	100.0	770	5	PCT-US95-17025-12
9	661	85.8	770	4	US-09-364-970-5
10	568	73.8	770	3	US-09-012-710-8
11	442	57.4	770	1	US-08-416-581B-9
12	221	28.7	770	1	US-08-416-581B-1
13	221	28.7	770	1	US-08-416-581B-5
14	221	28.7	770	4	US-09-087-465-6
15	221	28.7	771	1	US-08-276-099A-14
16	221	28.7	771	1	US-08-781-890-14
17	139	18.1	173	4	US-09-087-465-26
18	112	14.5	112	1	US-08-369-796-14
19	112	14.5	112	2	US-08-852-091-14
20	112	14.5	112	5	PCT-US95-17025-14
21	12	1.6	107	4	US-09-087-465-22
22	12	1.6	712	1	US-08-369-796-6
23	12	1.6	712	2	US-08-852-091-6
24	12	1.6	712	2	US-08-820-754-6
25	12	1.6	712	3	US-08-956-652-6
26	12	1.6	712	3	US-08-956-869-6
27	12	1.6	712	3	US-08-948-547-6

28	12	1.6	712	5	PCT-US95-17025-6	Sequence 6, Appli
29	12	1.6	740	1	US-08-276-099A-12	Sequence 12, Appli
30	12	1.6	740	1	US-08-781-890-12	Sequence 12, Appli
31	12	1.6	749	1	US-08-369-796-8	Sequence 8, Appli
32	12	1.6	749	2	US-08-852-091-8	Sequence 8, Appli
33	12	1.6	749	2	US-08-820-754-8	Sequence 8, Appli
34	12	1.6	749	3	US-08-956-652-8	Sequence 8, Appli
35	12	1.6	749	3	US-08-956-869-8	Sequence 8, Appli
36	12	1.6	749	3	US-09-012-710-7	Sequence 7, Appli
37	12	1.6	749	3	US-08-948-547-8	Sequence 8, Appli
38	12	1.6	749	5	PCT-US95-17025-8	Sequence 8, Appli
39	12	1.6	750	1	US-08-369-796-4	Sequence 4, Appli
40	12	1.6	750	2	US-08-852-091-4	Sequence 4, Appli
41	12	1.6	750	2	US-08-820-754-4	Sequence 4, Appli
42	12	1.6	750	3	US-08-956-652-4	Sequence 4, Appli
43	12	1.6	750	3	US-08-956-869-4	Sequence 4, Appli
44	12	1.6	750	3	US-08-948-547-4	Sequence 4, Appli
45	12	1.6	750	4	US-09-087-465-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-369-796-12  
; Sequence 12, Application US/08369796  
; Patent No. 5716622  
; GENERAL INFORMATION:  
; APPLICANT: James E. Darnell, Jr.  
; APPLICANT: Zilong Wen  
; APPLICANT: Curt M. Horvath  
; APPLICANT: Zhong Zhong  
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/369,796  
; FILING DATE: 06-JAN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-116  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 770 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-369-796-12

Query Match 100.0%; Score 770; DB 1; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOWNQLQDLTRYLKQLHQLYSDTFPMELOFLAPWIESQDMAYAAKESHATLVFHNH 60



Db 601 KPGCTELLRFSSSEKGGVFTTWVKDISGKTQIQSVPEYTKQOLNMSFAEIMGYKIM 660  
Qy 661 DATNILVSPVLYLPDIPKEAEFGKCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720  
Db 661 DATNILVSPVLYLPDIPKEAEFGKCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720  
Qy 721 TIDLPMSPRTLDSLMQFGNGGAEPSAGGQFESLTFDMDLTSECATSPM 770  
Db 721 TIDLPMSPRTLDSLMQFGNGGAEPSAGGQFESLTFDMDLTSECATSPM 770

RESULT 3  
US-08-820-754-12  
: Sequence 12, Application US/08820754  
: Patent No. 5976835  
: GENERAL INFORMATION:  
: APPLICANT: Darnell Jr., James E.  
: APPLICANT: Schindler, Christian W.  
: APPLICANT: Fu, Xian-Yuan  
: APPLICANT: Wen, Zilong  
: TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN  
: NUMBER OF SEQUENCES: 25  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Klauber & Jackson  
: STREET: 411 Hackensack Avenue  
: CITY: Hackensack  
: STATE: New Jersey  
: COUNTRY: USA  
: ZIP: 07601

: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/820,754  
: FILING DATE: 19-MAR-1997  
: CLASSIFICATION: 530  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/212,185  
: FILING DATE: 11-MAR-1994  
: APPLICATION NUMBER: US 07/980,498  
: FILING DATE: 23-NOV-1992

: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/854,296  
: FILING DATE: 19-MAR-1992  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: WO US93/02569  
: FILING DATE: 19-MAR-1993  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/126,588  
: FILING DATE: 24-SEP-1993  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Jackson Esq., David A.  
: REGISTRATION NUMBER: 26,742  
: REFERENCE/DOCKET NUMBER: 600-1-073 CIP  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 201 487-5800  
: TELEFAX: 201 343-1684  
: TELEX: 133521

: INFORMATION FOR SEQ ID NO: 12:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 770 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-08-820-754-12

Query Match 100.0%; Score 770; DB 2: Length 770;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAQWNOLOOLDTRYIKQLHQLYSDTFPMELROFLAPWIESODWAYAASKESHATLVFHNL 60  
Db 1 MAQWNOLOOLDTRYIKQLHQLYSDTFPMELROFLAPWIESODWAYAASKESHATLVFHNL 60  
Qy 61 LGEIDDOQYSRFLQESNVLYQHNLRIKQFLOSRYLEKPMETARIIVARCLWESRLQATA 120  
Db 61 LGEIDDOQYSRFLQESNVLYQHNLRIKQFLOSRYLEKPMETARIIVARCLWESRLQATA 120  
Qy 121 TAAQGGQGANHPTAAVTEKQOMLEQHLQDVVRKQVODLEQKMKVVENLQDDDFNYKTLK 180  
Db 121 TAAQGGQGANHPTAAVTEKQOMLEQHLQDVVRKQVODLEQKMKVVENLQDDDFNYKTLK 180  
Qy 181 SOGDMODLNGNOSVTRQKMOOLEQMLTALDOMRRSIVSELAGLISAMEYVOKTLTDEEL 240  
Db 181 SOGDMODLNGNOSVTRQKMOOLEQMLTALDOMRRSIVSELAGLISAMEYVOKTLTDEEL 240  
Qy 241 ADMKRPEIACIGGPNICLDRLNWTSLAESQLOTRQOIKKLEELOKVSYKGDPIVQ 300  
Db 241 ADMKRPLACIGGPNICLDRLNWTSLAESQLOTRQOIKKLEELOKVSYKGDPIVQ 300  
Qy 301 HRPMLERIVELFRNLMSAFVVEROPCPMPHDPRLVTKTGVQFTTKVRLLVKPELNY 360  
Db 301 HRPMLERIVELFRNLMSAFVVEROPCPMPHDPRLVTKTGVQFTTKVRLLVKPELNY 360  
Qy 361 OLKIKYCIDKDSGVAALRGSRKFNILGTNTKVMNNEESNNGSLSAFFKHLTLREORCN 420  
Db 361 OLKIKYCIDKDSGVAALRGSRKFNILGTNTKVMNNEESNNGSLSAFFKHLTLREORCN 420  
Qy 421 GGRANDASLIVTEELHLITFETEVYHQLKIDLETHSLPVVVISNICOMPNAWASILY 480  
Db 421 GGRANDASLIVTEELHLITFETEVYHQLKIDLETHSLPVVVISNICOMPNAWASILY 480  
Qy 481 NMLTNNPKVNFPTKPICTWDOVAEVLWSQFSSTTKRGLSTFQLTTLAEKLLGPGVNTS 540  
Db 481 NMLTNNPKVNFPTKPICTWDOVAEVLWSQFSSTTKRGLSTFQLTTLAEKLLGPGVNTS 540  
Qy 541 GCOITWAKFCCKENMAGKGFSPVWLDNIIDLKVKYIILALWNEGYIMGFISKERERAILST 600  
Db 541 GCOITWAKFCCKENMAGKGFSPVWLDNIIDLKVKYIILALWNEGYIMGFISKERERAILST 600  
Qy 601 KPGCTELLRFSSSEKGGVFTTWVKDISGKTQIQSVPEYTKQOLNMSFAEIMGYKIM 660  
Db 601 KPGCTELLRFSSSEKGGVFTTWVKDISGKTQIQSVPEYTKQOLNMSFAEIMGYKIM 660  
Qy 661 DATNILVSPVLYLPDIPKEAEFGKCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720  
Db 661 DATNILVSPVLYLPDIPKEAEFGKCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720  
Qy 721 TIDLPMSPRTLDSLMQFGNGGAEPSAGGQFESLTFDMDLTSECATSPM 770  
Db 721 TIDLPMSPRTLDSLMQFGNGGAEPSAGGQFESLTFDMDLTSECATSPM 770

RESULT 4  
US-08-956-652-12  
: Sequence 12, Application US/08956652  
: Patent No. 6013475  
: GENERAL INFORMATION:  
: APPLICANT: Darnell Jr., James E.  
: APPLICANT: Schindler, Christian W.  
: APPLICANT: Fu, Xian-Yuan  
: APPLICANT: Wen, Zilong  
: TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN  
: NUMBER OF SEQUENCES: 25  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Klauber & Jackson  
: STREET: 411 Hackensack Avenue  
: CITY: Hackensack  
: STATE: New Jersey

COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,652  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212,185  
FILING DATE: 11-MAR-1994  
APPLICATION NUMBER: US 07/980,498  
FILING DATE: 23-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/854,296  
FILING DATE: 19-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO US93/02569  
FILING DATE: 19-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/126,588  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-073 CIP  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 770 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-956-652-12

Query Match 100.0%; Score 770; DB 3; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNOLOQDTRYLKQHLQYSDTFPMLRQFLAPWIESODWAYAASKESHATLVFHNL 60  
DB 1 MAQWNOLOQDTRYLKQHLQYSDTFPMLRQFLAPWIESODWAYAASKESHATLVFHNL 60  
QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKOFLOSRYLEKPMETARIVARCLWEESRLQTA 120  
DB 61 LGEIDQOYSRFLQESNVLYQHNLRIKOFLOSRYLEKPMETARIVARCLWEESRLQTA 120  
QY 121 TAAQGGQANHPPTAAVTEKQOMLEOHLDQVYKRVODLEQKMKVYVENLQDDFDENYKTLK 180  
DB 121 TAAQGGQANHPPTAAVTEKQOMLEOHLDQVYKRVODLEQKMKVYVENLQDDFDENYKTLK 180  
QY 181 SGQDMQDLNCGNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLSAMEYVOKLTLDDEL 240  
DB 181 SGQDMQDLNCGNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLSAMEYVOKLTLDDEL 240  
QY 241 ADWKRPEIACIGGPNICLDLENWITSLAESOLQTRQOIKKLELOOKYSYKGDPIVQ 300  
DB 241 ADWKRPEIACIGGPNICLDLENWITSLAESOLQTRQOIKKLELOOKYSYKGDPIVQ 300  
QY 301 HRPMLEERIVELFRNLMSAFVVERQPCMPHMPDRPLVIKTGVQFTTKVRLLVKFPPELNY 360  
DB 301 HRPMLEERIVELFRNLMSAFVVERQPCMPHMPDRPLVIKTGVQFTTKVRLLVKFPPELNY 360  
QY 361 QLKIKVICDKSDVAALRGSRKFNILGTNTKVMNWEESNNGSLSAEPKHLTLRQRCGN 420  
DB 361 QLKIKVICDKSDVAALRGSRKFNILGTNTKVMNWEESNNGSLSAEPKHLTLRQRCGN 420

QY 421 GGRANDASLIVTEELHLITETEVYHOGKLIDLETHSLPVVVISNICOMPANASILWY 480  
DB 421 GGRANDASLIVTEELHLITETEVYHOGKLIDLETHSLPVVVISNICOMPANASILWY 480  
QY 481 NMLTNNPKNVNFFTKPPIGTWDOVAEVLWSQFSSSTTKRGLSIEQLTTTAEKLLGPGVNY 540  
DB 481 NMLTNNPKNVNFFTKPPIGTWDOVAEVLWSQFSSSTTKRGLSIEQLTTTAEKLLGPGVNY 540  
QY 541 GCOITWAKFCKENMAGKGFSSFWWLDNIIDLKVKYILALWNEGYIMGFISKERAILST 600  
DB 541 GCOITWAKFCKENMAGKGFSSFWWLDNIIDLKVKYILALWNEGYIMGFISKERAILST 600  
QY 601 KPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIOSVEPYTKQQLNNMSFAEIMGYKIM 660  
DB 601 KPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIOSVEPYTKQQLNNMSFAEIMGYKIM 660  
QY 661 DATNLLVSPVLVLYPDIPKEAFGKYCRPESOEHPADGSAAPYLKTKFCVTPPTCSN 720  
DB 661 DATNLLVSPVLVLYPDIPKEAFGKYCRPESOEHPADGSAAPYLKTKFCVTPPTCSN 720  
QY 721 TIDLPMSPRTLDSLMQFGNNGEAPSGAGGFESI.TFMDLITSECATSPM 770  
DB 721 TIDLPMSPRTLDSLMQFGNNGEAPSGAGGFESI.TFMDLITSECATSPM 770

RESULT 5  
US-08-956-869-12  
Sequence 12, Application US/08956869  
Patent No. 6030808  
GENERAL INFORMATION:  
APPLICANT: Darnell Jr., James E.  
APPLICANT: Schindler, Christian W.  
APPLICANT: Fu, Xian-Yuan  
APPLICANT: Wen, Zilong  
APPLICANT: Zhong, Zhong  
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,869  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/212,185  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/854,296  
FILING DATE: 19-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO US93/02569  
FILING DATE: 19-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/126,588  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-073 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800



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; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 770 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-956-869-12

Query Match      100.0%; Score 770; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MAQWNOLOOLDTRYLKQLHOLYSDTFPMELOFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MAQWNOLOOLDTRYLKQLHOLYSDTFPMELOFLAPWIESQDWAYAASKESHATLVFHNL 60
Oy 61 LGEIDQOYSRFLQESNVLYOHNLRRIKQFLOSRYLEKPMETARIVARCLWESRLLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYOHNLRRIKQFLOSRYLEKPMETARIVARCLWESRLLQTAA 120
Oy 121 TAAQOQGGQANHPHTAAVVTKEQOQMLEQHLQDQVRKRVODLEQKMKVVENLODDDFNFKTLK 180
Db 121 TAAQOQGGQANHPHTAAVVTKEQOQMLEQHLQDQVRKRVODLEQKMKVVENLODDDFNFKTLK 180
Oy 181 SOGDMODLNGNOSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMYVOKTLTDEEL 240
Db 181 SOGDMODLNGNOSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMYVOKTLTDEEL 240
Oy 241 ADKRRPEIACIGPPNICDLRENMTSLAESQLQTRQOIKKLEEOQKVSYGKDPVQ 300
Db 241 ADKRRPEIACIGPPNICDLRENMTSLAESQLQTRQOIKKLEEOQKVSYGKDPVQ 300
Oy 301 HRPMLERIVELFRNLKSAFVVEROPCPMPHDPRLVTKTGVQFTKVRLLVKPELNY 360
Db 301 HRPMLERIVELFRNLKSAFVVEROPCPMPHDPRLVTKTGVQFTKVRLLVKPELNY 360
Oy 361 QLKIKVICDKSDGVAALRGSRKFNILGTNTKVMNNEESNNGSLSAEPKHLTLREQRCN 420
Db 361 QLKIKVICDKSDGVAALRGSRKFNILGTNTKVMNNEESNNGSLSAEPKHLTLREQRCN 420
Oy 421 GGRANDASLIIVTEELHLITFETEVYHOGKIDLETHSLPVPVVISNICOMPNAWASILMY 480
Db 421 GGRANDASLIIVTEELHLITFETEVYHOGKIDLETHSLPVPVVISNICOMPNAWASILMY 480
Oy 481 NMLTNPKNVNFTKPPIGTWQDQVAEVLWSQFSTTKRGLSIEQLTTLAEKLLGPCVNY 540
Db 481 NMLTNPKNVNFTKPPIGTWQDQVAEVLWSQFSTTKRGLSIEQLTTLAEKLLGPCVNY 540
Oy 541 GCQITWAKFKCKENMACKGFSFWWLDNIIDLKVKYILALWNEGYIMGFISKERAILST 600
Db 541 GCQITWAKFKCKENMACKGFSFWWLDNIIDLKVKYILALWNEGYIMGFISKERAILST 600
Oy 601 KPCTELLRSESSKGGVFTTWKXDISGKTQIQSVETPYTKOOLNMMSFAELIMCYKIM 660
Db 601 KPCTELLRSESSKGGVFTTWKXDISGKTQIQSVETPYTKOOLNMMSFAELIMCYKIM 660
Oy 661 DATNILVSPVLVLYPDIPKEAFGKCRPESQHPHPCGSAAPYLUKTKFTICVPTTCSN 720
Db 661 DATNILVSPVLVLYPDIPKEAFGKCRPESQHPHPCGSAAPYLUKTKFTICVPTTCSN 720
Oy 721 TIDLPMSPRTLDSLMQFGNGEGAFPSAGQFESLTFDMDLTSECATSPM 770
Db 721 TIDLPMSPRTLDSLMQFGNGEGAFPSAGQFESLTFDMDLTSECATSPM 770

RESULT 6
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:

; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 770 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-948-547-12

Query Match      100.0%; Score 770; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MAQWNOLOOLDTRYLKQLHOLYSDTFPMELOFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MAQWNOLOOLDTRYLKQLHOLYSDTFPMELOFLAPWIESQDWAYAASKESHATLVFHNL 60
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Db 61 LGEIDQOYSRFLQESNVLYOHNLRRIKQFLOSRYLEKPMETARIVARCLWESRLLQTAA 120
Oy 121 TAAQOQGGQANHPHTAAVVTKEQOQMLEQHLQDQVRKRVODLEQKMKVVENLODDDFNFKTLK 180
Db 121 TAAQOQGGQANHPHTAAVVTKEQOQMLEQHLQDQVRKRVODLEQKMKVVENLODDDFNFKTLK 180
Oy 181 SOGDMODLNGNOSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMYVOKTLTDEEL 240
Db 181 SOGDMODLNGNOSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMYVOKTLTDEEL 240
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Db 181 SOGDMODLNGNNSVTRQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVOKTLTDEEL 240  
QY 241 ADWKRPEIACIGGPNICLDRLENWITSLSAESQLOTRQOIKKLEELQOKVSYKGDPIVQ 300  
Db 241 ADWKRPEIACIGGPNICLDRLENWITSLSAESQLOTRQOIKKLEELQOKVSYKGDPIVQ 300  
QY 301 HRPMLERIVELFRNLMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPELNY 360  
Db 301 HRPMLERIVELFRNLMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPELNY 360  
QY 361 QLKIKVCIDKSDGVAALRGSRKFNLGTNTKVMNMEESNNGSLSAEFKHLTLREORCGN 420  
Db 361 QLKIKVCIDKSDGVAALRGSRKFNLGTNTKVMNMEESNNGSLSAEFKHLTLREORCGN 420  
QY 421 GGRANCASLIIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILWY 480  
Db 421 GGRANCASLIIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILWY 480  
QY 481 NMLTNNPKNVNFTKPPITGTDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540  
Db 481 NMLTNNPKNVNFTKPPITGTDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540  
QY 541 GCOITWAKFCKENMAGKGFSPWWLDNIIDLKVKYILALWNEGYIMGFISKERERAILST 600  
Db 541 GCOITWAKFCKENMAGKGFSPWWLDNIIDLKVKYILALWNEGYIMGFISKERERAILST 600  
QY 601 KPPGTFLLRFSSESSKEGGVFTTWVEKDLSGKTQIOSVEPYTKOQLNNMSFAEIIIMGYKIM 660  
Db 601 KPPGTFLLRFSSESSKEGGVFTTWVEKDLSGKTQIOSVEPYTKOQLNNMSFAEIIIMGYKIM 660  
QY 661 DATNILVSPVLYLPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFCIVTPTTCSN 720  
Db 661 DATNILVSPVLYLPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFCIVTPTTCSN 720  
QY 721 TIDLPMSPRTLDSLMQFGNNGEAGPESAGGQFESLTFDMDLTSECATSPM 770  
Db 721 TIDLPMSPRTLDSLMQFGNNGEAGPESAGGQFESLTFDMDLTSECATSPM 770  
RESULT 7  
US-09-364-970-3  
; Sequence 3, Application US/09364970  
; Patent No. 6235873  
; GENERAL INFORMATION:  
; APPLICANT: Bromberg, Jacqueline  
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR  
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING  
; TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES  
; FILE REFERENCE: 600-1-252  
; CURRENT APPLICATION NUMBER: US/09/364,970  
; CURRENT FILING DATE: 1999-07-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-364-970-3  
Query Match 100.0%; Score 770; DB 4; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAONHLOOLDTRYLKOLHQLYSDTFPMELRQFLAPHIESQDWAYAASKESHATLVPHNL 60  
Db 1 MAONHLOOLDTRYLKOLHQLYSDTFPMELRQFLAPHIESQDWAYAASKESHATLVPHNL 60  
QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLOSRYLEKPMETARIVARCLWEESRLQTAA 120  
Db 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLOSRYLEKPMETARIVARCLWEESRLQTAA 120  
QY 121 TAAOQGOANHPTAAVVTKEQMLEQHLQDVRKRVQDLEOKMKVVENLQDDDFNFKTLK 180

Db 121 TAAOQGOANHPTAAVVTKEQMLEQHLQDVRKRVQDLEOKMKVVENLQDDDFNFKTLK 180  
QY 181 SOGDMODLNGNNSVTRQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVOKTLTDEEL 240  
Db 181 SOGDMODLNGNNSVTRQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVOKTLTDEEL 240  
QY 241 ADWKRPEIACIGGPNICLDRLENWITSLSAESQLOTRQOIKKLEELQOKVSYKGDPIVQ 300  
Db 241 ADWKRPEIACIGGPNICLDRLENWITSLSAESQLOTRQOIKKLEELQOKVSYKGDPIVQ 300  
QY 301 HRPMLERIVELFRNLMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPELNY 360  
Db 301 HRPMLERIVELFRNLMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPELNY 360  
QY 361 QLKIKVCIDKSDGVAALRGSRKFNLGTNTKVMNMEESNNGSLSAEFKHLTLREORCGN 420  
Db 361 QLKIKVCIDKSDGVAALRGSRKFNLGTNTKVMNMEESNNGSLSAEFKHLTLREORCGN 420  
QY 421 GGRANCASLIIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILWY 480  
Db 421 GGRANCASLIIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILWY 480  
QY 481 NMLTNNPKNVNFTKPPITGTDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540  
Db 481 NMLTNNPKNVNFTKPPITGTDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540  
QY 541 GCOITWAKFCKENMAGKGFSPWWLDNIIDLKVKYILALWNEGYIMGFISKERERAILST 600  
Db 541 GCOITWAKFCKENMAGKGFSPWWLDNIIDLKVKYILALWNEGYIMGFISKERERAILST 600  
QY 601 KPPGTFLLRFSSESSKEGGVFTTWVEKDLSGKTQIOSVEPYTKOQLNNMSFAEIIIMGYKIM 660  
Db 601 KPPGTFLLRFSSESSKEGGVFTTWVEKDLSGKTQIOSVEPYTKOQLNNMSFAEIIIMGYKIM 660  
QY 661 DATNILVSPVLYLPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFCIVTPTTCSN 720  
Db 661 DATNILVSPVLYLPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFCIVTPTTCSN 720  
QY 721 TIDLPMSPRTLDSLMQFGNNGEAGPESAGGQFESLTFDMDLTSECATSPM 770  
Db 721 TIDLPMSPRTLDSLMQFGNNGEAGPESAGGQFESLTFDMDLTSECATSPM 770  
RESULT 8  
PCT-US95-17025-12  
; Sequence 12, Application PC/TUS9517025  
; GENERAL INFORMATION:  
; APPLICANT: James E. Darnell, Jr.  
; APPLICANT: Zilong Wen  
; APPLICANT: Curt M. Horvath  
; APPLICANT: Zhong Zhong  
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17025  
; FILING DATE: 28-DEC-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/369,796

FILING DATE: 06-JAN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 770 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-17025-12

Query Match 100.0%; Score 770; DB 5; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNOLOQLDTRYLKQLHQLYSDFPMELOFAPWIESQDWAYAASKESHATLVFHNL 60  
DB 1 MAQWNOLOQLDTRYLKQLHQLYSDFPMELOFAPWIESQDWAYAASKESHATLVFHNL 60  
QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLOSRYLEKPMELIARIVARCLWEESRLQATA 120  
DB 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLOSRYLEKPMELIARIVARCLWEESRLQATA 120  
QY 121 TAAQGGQGANHPTAAVYTEKQOQLEHQLQDVRRKRVODLEQKMKVVENLQDDDFDNFKTLK 180  
DB 121 TAAQGGQGANHPTAAVYTEKQOQLEHQLQDVRRKRVODLEQKMKVVENLQDDDFDNFKTLK 180  
QY 181 SQGDMODLNGNQSVTRQKMOQLEOMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEEL 240  
DB 181 SQGDMODLNGNQSVTRQKMOQLEOMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEEL 240  
QY 241 ADWKRPEIACIGGPNICLDRLNNWITSLSAESOLQTRQOIKKLEELQOQVSYKGDPIVQ 300  
DB 241 ADWKRPEIACIGGPNICLDRLNNWITSLSAESOLQTRQOIKKLEELQOQVSYKGDPIVQ 300  
QY 301 HRPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTVQVFTTKVRLLVKFPPELNY 360  
DB 301 HRPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTVQVFTTKVRLLVKFPPELNY 360  
QY 361 QLKIKVCIDKSDGVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHILTLRQRCGN 420  
DB 361 QLKIKVCIDKSDGVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHILTLRQRCGN 420  
QY 421 GGRANDASLIVTEELHLITFETEVYHOGKIDLETHSLPVPVVISNICOMPNAWASILMY 480  
DB 421 GGRANDASLIVTEELHLITFETEVYHOGKIDLETHSLPVPVVISNICOMPNAWASILMY 480  
QY 481 NMLTNPKNVNFFTKPPIGTWDOVAEVLWSQFSSTTKRGLSIEQLTTLAELKLLPGVNY 540  
DB 481 NMLTNPKNVNFFTKPPIGTWDOVAEVLWSQFSSTTKRGLSIEQLTTLAELKLLPGVNY 540  
QY 541 GCOITWAKFCENKMGAGKFSFWWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST 600  
DB 541 GCOITWAKFCENKMGAGKFSFWWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST 600  
QY 601 KPGTFTLLRFSSESSKEGGVFTTWVEKDISGKTQIOSVEPYTKQOLNNNSFAEIMGYKIM 660  
DB 601 KPGTFTLLRFSSESSKEGGVFTTWVEKDISGKTQIOSVEPYTKQOLNNNSFAEIMGYKIM 660  
QY 661 DATNILVPLVLYLVDIPKEEAFGKYCRPESQHPADPGSAAPYLKTKFICVTPPTCSN 720  
DB 661 DATNILVPLVLYLVDIPKEEAFGKYCRPESQHPADPGSAAPYLKTKFICVTPPTCSN 720  
QY 721 TIDLPMSPRTLDSLMOFGNNGEAGPSAGQGFESLTFDMDLTSECATSPM 770  
DB 721 TIDLPMSPRTLDSLMOFGNNGEAGPSAGQGFESLTFDMDLTSECATSPM 770

Db 721 TIDLPMSPRTLDSLMOFGNNGEAGPSAGQGFESLTFDMDLTSECATSPM 770

RESULT 9  
US-09-364-970-5  
; Sequence 5, Application US/09364970  
; Patent No. 6235873  
; GENERAL INFORMATION:  
; APPLICANT: Bromberg, Jacqueline  
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR  
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING  
; TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES  
; FILE REFERENCE: 600-1-252  
; CURRENT APPLICATION NUMBER: US/09/364,970  
; CURRENT FILING DATE: 1999-07-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Macintosh Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-364-970-5

Query Match 85.8%; Score 661; DB 4; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNOLOQLDTRYLKQLHQLYSDFPMELOFAPWIESQDWAYAASKESHATLVFHNL 60  
DB 1 MAQWNOLOQLDTRYLKQLHQLYSDFPMELOFAPWIESQDWAYAASKESHATLVFHNL 60  
QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLOSRYLEKPMELIARIVARCLWEESRLQATA 120  
DB 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLOSRYLEKPMELIARIVARCLWEESRLQATA 120  
QY 121 TAAQGGQGANHPTAAVYTEKQOQLEHQLQDVRRKRVODLEQKMKVVENLQDDDFDNFKTLK 180  
DB 121 TAAQGGQGANHPTAAVYTEKQOQLEHQLQDVRRKRVODLEQKMKVVENLQDDDFDNFKTLK 180  
QY 181 SQGDMODLNGNQSVTRQKMOQLEOMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEEL 240  
DB 181 SQGDMODLNGNQSVTRQKMOQLEOMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEEL 240  
QY 241 ADWKRPEIACIGGPNICLDRLNNWITSLSAESOLQTRQOIKKLEELQOQVSYKGDPIVQ 300  
DB 241 ADWKRPEIACIGGPNICLDRLNNWITSLSAESOLQTRQOIKKLEELQOQVSYKGDPIVQ 300  
QY 301 HRPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTVQVFTTKVRLLVKFPPELNY 360  
DB 301 HRPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTVQVFTTKVRLLVKFPPELNY 360  
QY 361 QLKIKVCIDKSDGVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHILTLRQRCGN 420  
DB 361 QLKIKVCIDKSDGVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHILTLRQRCGN 420  
QY 421 GGRANDASLIVTEELHLITFETEVYHOGKIDLETHSLPVPVVISNICOMPNAWASILMY 480  
DB 421 GGRANDASLIVTEELHLITFETEVYHOGKIDLETHSLPVPVVISNICOMPNAWASILMY 480  
QY 481 NMLTNPKNVNFFTKPPIGTWDOVAEVLWSQFSSTTKRGLSIEQLTTLAELKLLPGVNY 540  
DB 481 NMLTNPKNVNFFTKPPIGTWDOVAEVLWSQFSSTTKRGLSIEQLTTLAELKLLPGVNY 540  
QY 541 GCOITWAKFCENKMGAGKFSFWWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST 600  
DB 541 GCOITWAKFCENKMGAGKFSFWWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST 600  
QY 601 KPGTFTLLRFSSESSKEGGVFTTWVEKDISGKTQIOSVEPYTKQOLNNNSFAEIMGYKIM 660  
DB 601 KPGTFTLLRFSSESSKEGGVFTTWVEKDISGKTQIOSVEPYTKQOLNNNSFAEIMGYKIM 660  
QY 661 D 661

241	Db	ADWKRRQQTACIGGPPNICDLRLENWITS	LAESQLOTRQIQKKLELQOKVSYKGDP	PIVQ	300
301	Qy	HRPMLERIVELFRNLMSAFVVEROPCP	MPHDPRLVTKTGVQFTTKVRLLVKPE	PELNY	360
301	Db	HRPMLERIVELFRNLMSAFVVEROPCP	MPHDPRLVTKTGVQFTTKVRLLVKPE	PELNY	360
361	Qy	QLKIKVICDKSGDVAALRGSRKFNLT	NTKVMNMEESNNGSLSAEPKHLTLR	QORCGN	420
361	Db	QLKIKVICDKSGDVAALRGSRKFNLT	NTKVMNMEESNNGSLSAEPKHLTLR	QORCGN	420
421	Qy	GGRANDASLIVTEELHLTLTFETEVY	HQGLKIDLETHSLPVVVISINICOMP	NAWASILMY	480
421	Db	GGRANDASLIVTEELHLTLTFETEVY	HQGLKIDLETHSLPVVVISINICOMP	NAWASILMY	480
481	Qy	NMLTNPNKNVFFTKPIGTWDOVAEVL	SWQFSSTTKRGLSIEQLTTLAEKLL	GPCVNY	540
481	Db	NMLTNPNKNVFFTKPIGTWDOVAEVL	SWQFSSTTKRGLSIEQLTTLAEKLL	GPCVNY	540
541	Qy	GCQITWAKCKENMACKGFSFWWLDNI	IIDLVKKYILALWNKGYIMGFI	SKRERAILST	600
541	Db	GCQITWAKCKENMACKGFSFWWLDNI	IIDLVKKYILALWNKGYIMGFI	SKRERAILST	600
601	Qy	KPGCTFLLRFSESSKEGGVFTTWVK	DKDISGKTQIOSVEPYTKOOLNMS	FAEIIIMGYKIM	660
601	Db	KPGCTFLLRFSESSKEGGVFTTWVK	DKDISGKTQIOSVEPYTKOOLNMS	FAEIIIMGYKIM	660
661	Qy	DATNILVSPLYVYDPIKPEEAFGKY	CRPESQBHPADPGSAAPYIKTKTF	ICVTPTTCSN	720
661	Db	DATNILVSPLYVYDPIKPEEAFGKY	CRPESQBHPADPGSAAPYIKTKTF	ICVTPTTCSN	720
721	Qy	TIDLPMSPRTLDSLMQFGNGGCAE	PSAGGQFESLTFDMDLTSECATS	SPM	770
721	Db	TIDLPMSPRTLDSLMQFGNGGCAE	PSAGGQFESLTFDMDLTSECATS	SPM	770
RESULT 11					
US-08-416-5819-9					
: Sequence 9, Application US/08416581B					
: Patent No. 5719042					
: GENERAL INFORMATION:					
: APPLICANT: Kishimoto, Tadimitsu					
: APPLICANT: Akira, Shizuo					
: TITLE OF INVENTION: TRANSCRIPTION FACTOR APFR					
: NUMBER OF SEQUENCES: 11					
: CORRESPONDENCE ADDRESS:					
: ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS					
: STREET: 2100 Pennsylvania Avenue, N.W.					
: CITY: Washington					
: STATE: D.C.					
: COUNTRY: USA					
: ZIP: 20037					
: COMPUTER READABLE FORM:					
: MEDIUM TYPE: Floppy disk					
: COMPUTER: IBM PC compatible					
: OPERATING SYSTEM: PC-DOS/MS-DOS					
: SOFTWARE: Patentin Release #1.0, Version #1.30					
: CURRENT APPLICATION DATA:					
: APPLICATION NUMBER: US/08/416,581B					
: FILING DATE: 04-APR-1995					
: CLASSIFICATION: 435					
: PRIOR APPLICATION DATA:					
: APPLICATION NUMBER: JP 6-65825/1994					
: FILING DATE: 04-APR-1994					
: ATTORNEY/AGENT INFORMATION:					
: NAME: Nakamura, Dean H.					
: REGISTRATION NUMBER: 33,981					
: REFERENCE/DOCKET NUMBER: Q-37891					
: TELECOMMUNICATION INFORMATION:					
: TELEPHONE: (202)293-7060					
: TELEFAX: (202)293-7860					
: INFORMATION FOR SEQ ID NO: 9:					
: SEQUENCE CHARACTERISTICS:					
: LENGTH: 770 amino acids					

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-416-581B-9

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Query Match	57.4%	Score 442:	DB 1:	Length 770:		
Best Local Similarity	99.6%	Pred. No. 0:				
Matches 742:	Conservative	0:	Mismatches	3: Indels	0: Gaps	0:
QY	26	FMPELROFLAPWIESODWAYAASKESSHATLVFHNLLGEIDQOYSRFLQSNVLYOHNLRR	85			
Db	26	FMPELROFLAPWIESODWAYAASKESSHATLVFHNLLGEIDQOYSRFLQSNVLYOHNLRR	85			
QY	86	IKOFLQSRYLEKPMIEARIVARCLWEESRLQTAATAAQOGGOANHPTAAVYTERQOQMLE	145			
Db	86	IKOFLQSRYLEKPMIEARIVARCLWEESRLQTAATAAQOGGOANHPTAAVYTERQOQMLE	145			
QY	146	QHLQDVRKRVODLEOKMKVVENLODDDFNYKTLKSQDQMODLNGNQSVTRKQWOOLEQ	205			
Db	146	QHLQDVRKRVODLEOKMKVVENLODDDFNYKTLKSQDQMODLNGNQSVTRKQWOOLEQ	205			
QY	206	MLTALDQMRRSIVSELAGLLSAMEYVOKLTUDEADWKRRPFIACIGGPPNICLDRLN	265			
Db	206	MLTALDQMRRSIVSELAGLLSAMEYVOKLTUDEADWKRRQOJACIGGPPNICLDRLN	265			
QY	266	WITSLAESOLQTOOIKKLELOQKVSYGDPITVOHRPMLEERIVELFRNLKMSAFVVER	325			
Db	266	WITSLAESOLQTOOIKKLELOQKVSYGDPITVOHRPMLEERIVELFRNLKMSAFVVER	325			
QY	326	QPCMPMHPDRPLVKTGVQFTTKVRLVLVKPELNYQLKIKVCIDKDSGDVAAALRGRKEN	385			
Db	326	QPCMPMHPDRPLVKTGVQFTTKVRLVLVKPELNYQLKIKVCIDKDSGDVAAALRGRKEN	385			
QY	386	ILGTNTKYNMNEESNNGSLSAEFKHLTLRQRCGNGGRANCDSLIVTEELHLITFETEV	445			
Db	386	ILGTNTKYINNEESNNGSLSAEFKHLTLRQRCGNGGRANCDSLIVTEELHLITFETEV	445			
QY	446	YHOGLKIDLETHSLDPVVISNICOMPANAWASILWYNMLTNPNKNVNFYFKPIGTWDQVA	505			
Db	446	YHOGLKIDLETHSLDPVVVISNICOMPANAWASILWYNMLTNPNKNVNFYFKPIGTWDQVA	505			
QY	506	EVLWSQFSTTKRGLSIEBOLTTAEKLLGPGVNYSGCOITWAKFCENMAGGFSFWYWL	565			
Db	506	EVLWSQFSTTKRGLSIEBOLTTAEKLLGPGVNYSGCOITWAKFCENMAGGFSFWYWL	565			
QY	566	DNIIDLWKYIILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVFTTWE	625			
Db	566	DNIIDLWKYIILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVFTTWE	625			
QY	626	KDLSCKTOIQSVEPYTKOOLNNMSFAEIMGYKIMDATNITLVSPLYLYLPDIPKEAFGK	685			
Db	626	KDLSCKTOIQSVEPYTKOOLNNMSFAEIMGYKIMDATNITLVSPLYLYLPDIPKEAFGK	685			
QY	686	YCRPESQEHPEADPGSAAPYLKTKFICVPTTCSNTIDLPMSPRTLDLSMQFNNGEAAE	745			
Db	686	YCRPESQEHPEADPGSAAPYLKTKFICVPTTCSNTIDLPMSPRTLDLSMQFNNGEAAE	745			
QY	746	PSAGGOFESLTFDMDLTSECATSPM	770			
Db	746	PSAGGOFESLTFDMDLTSECATSPM	770			

RESULT 12  
US-08-416-581B-1  
: Sequence 1, Application US/08416581B  
: Patent No. 5719042  
: GENERAL INFORMATION:  
: APPLICANT: Kishimoto, Tadamitsu  
: APPLICANT: Akira, Shizuo  
: TITLE OF INVENTION: TRANSCRIPTION FACTOR APRE  
: NUMBER OF SEQUENCES: 11  
: CORRESPONDENCE ADDRESSES:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release 1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/416,581B  
FILING DATE: 04-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-65825/1994  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Dean H.  
REGISTRATION NUMBER: 33,981  
REFERENCE/DOCKET NUMBER: Q-37891  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 770 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-416-581B-1

Query Match 28.7%; Score 221; DB 1; Length 770;  
Best Local Similarity 100.0%; Pred. No. 3.1e-197;  
Matches 221; Conservative 0; Mismatches 0; Indels

[illegible]

```

RESULT 13
US-08-416-581B-5
; Sequence 5, Application US/08416581B
; Patent No. 5719042
; GENERAL INFORMATION:
; APPLICANT: Kishimoto, Tadamitsu
; APPLICANT: Akira, Shizuo
; TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,581B
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-65825/1994
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: O-37891
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-416-581B-5

Query Match      28.7%; Score 221; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.1e-197;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLRR 85
DB 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLRR 85
QY 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
DB 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
QY 146 QHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMODLNGNNSVTRKMOOLEQ 205
DB 146 QHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMODLNGNNSVTRKMOOLEQ 205
QY 206 MLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRR 246
DB 206 MLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRR 246

RESULT 15
US-08-276-099A-14
; Sequence 14, Application US/08276099A
; Patent No. 5591825
; GENERAL INFORMATION:
; APPLICANT: McKnight, Steven L
; APPLICANT: Hou, Jinzhao
; TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND
; TITLE OF INVENTION: BINDING ASSAYS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,099A
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard Aron
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59451-1/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 398-3249
; TELEFAX: (415) 398-3249
; TELEFAX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-276-099A-14

Query Match      28.7%; Score 221; DB 1; Length 771;
Best Local Similarity 100.0%; Pred. No. 3.1e-197;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLRR 85
DB 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLRR 85
QY 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
DB 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145

Query Match      28.7%; Score 221; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.1e-197;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,465A
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-65825/1994
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: O-37891
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-416-581B-5

Query Match      28.7%; Score 221; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.1e-197;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLRR 85
DB 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLRR 85
QY 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
DB 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
QY 146 QHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMODLNGNNSVTRKMOOLEQ 205
DB 146 QHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMODLNGNNSVTRKMOOLEQ 205
QY 206 MLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRR 246
DB 206 MLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRR 246

RESULT 14
US-09-087-465-6
; Sequence 6, Application US/09087465A
; Patent No. 6160092
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Chen, Xiaomin
; APPLICANT: Darnell Jr., James E
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 600-1-229
; CURRENT APPLICATION NUMBER: US/09/087,465A
; CURRENT FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-087-465-6

Query Match      28.7%; Score 221; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.1e-197;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLRR 85
DB 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLRR 85
QY 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
DB 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
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Db 86 IKQFLOSRYLEKPMPIARIVARCLWEESRLQTAATAAQOQOANHPTAAVVTKEQOMLE 145  
Qy 146 QHLQDVRRKRVODLEOKMKVVENLQDDDFNFYKTLKSGQMDLNGNNSVTRQKMOOLEQ 205  
Db 146 QHLQDVRRKRVODLEOKMKVVENLQDDDFNFYKTLKSGQMDLNGNNSVTRQKMOOLEQ 205  
Qy 206 MTLALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 246  
Db 206 MTLALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 246  
RESULT 16  
US-08-781-890-14  
: Sequence 14, Application US/08781890  
: Patent No. 5710266  
: GENERAL INFORMATION:  
: APPLICANT: McKnight, Steven L  
: APPLICANT: Hou, Jinzhao  
: TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND  
: TITLE OF INVENTION: BINDING ASSAYS  
: NUMBER OF SEQUENCES: 17  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: FLEHR, ROHBACH, TEST, ALBRITTON & HERBERT  
: STREET: 4 Embarcadero Center, Suite 3400  
: CITY: San Francisco  
: STATE: California  
: COUNTRY: USA  
: ZIP: 94111-4187  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/781,890  
: FILING DATE: 05-JAN-1997  
: CLASSIFICATION: 536  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/276,099  
: FILING DATE: 15-JUL-1994  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Osman, Richard Aron  
: REGISTRATION NUMBER: 36,627  
: REFERENCE/DOCKET NUMBER: A-59451-1/RAO  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (415) 781-1989  
: TELEFAX: (415) 398-3249  
: TELEX: 910 277299  
: INFORMATION FOR SEQ ID NO: 14:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 771 amino acids  
: TYPE: amino acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: peptide  
US-08-781-890-14  
Query Match 28.7%; Score 221; DB 1; Length 771;  
Best Local Similarity 100.0%; Pred. No. 3,1e-197;  
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 26 FPMELRQFLAPWIESQDWAYAASKEASHATLVFHNLLGELIDQOYSRFLQESNVLYOHNLR 85  
Db 26 FPMELRQFLAPWIESQDWAYAASKEASHATLVFHNLLGELIDQOYSRFLQESNVLYOHNLR 85  
Qy 86 IKQFLOSRYLEKPMPIARIVARCLWEESRLQTAATAAQOQOANHPTAAVVTKEQOMLE 145  
Db 86 IKQFLOSRYLEKPMPIARIVARCLWEESRLQTAATAAQOQOANHPTAAVVTKEQOMLE 145  
Qy 146 QHLQDVRRKRVODLEOKMKVVENLQDDDFNFYKTLKSGQMDLNGNNSVTRQKMOOLEQ 205  
Db 146 QHLQDVRRKRVODLEOKMKVVENLQDDDFNFYKTLKSGQMDLNGNNSVTRQKMOOLEQ 205

Qy 206 MTLALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 246  
Db 206 MTLALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 246  
RESULT 17  
US-09-087-465-26  
: Sequence 26, Application US/09087465A  
: Patent No. 6160092  
: GENERAL INFORMATION:  
: APPLICANT: Vinkemeier, Uwe  
: APPLICANT: Chen, Xiaomin  
: APPLICANT: Darnell Jr., James E  
: APPLICANT: Kuriyama, John  
: TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS OF  
: TITLE OF INVENTION: USE  
: FILE REFERENCE: 600-1-229  
: CURRENT APPLICATION NUMBER: US/09/087,465A  
: CURRENT FILING DATE: 1998-05-29  
: NUMBER OF SEQ ID NOS: 37  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 26  
: LENGTH: 173  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-087-465-26  
Query Match 18.1%; Score 139; DB 4; Length 173;  
Best Local Similarity 100.0%; Pred. No. 1.6e-121;  
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 321 FVVERQPCMPHDPRLVIVKTVQFTTKVRLVVKFPELVQKIKVICDKSDGVAALRG 380  
Db 1 FVVERQPCMPHDPRLVIVKTVQFTTKVRLVVKFPELVQKIKVICDKSDGVAALRG 60  
Qy 381 SRKFNLGTNTKVMNEESNNGSLSAEFKHLTLREORCGNGRANCDAASLIVTEELHLIT 440  
Db 61 SRKFNLGTNTKVMNEESNNGSLSAEFKHLTLREORCGNGRANCDAASLIVTEELHLIT 120  
Qy 441 FETEVYHQLKIDLETHSL 459  
Db 121 FETEVYHQLKIDLETHSL 139  
RESULT 18  
US-08-369-796-14  
: Sequence 14, Application US/08369796  
: Patent No. 5716622  
: GENERAL INFORMATION:  
: APPLICANT: James E. Darnell, Jr.  
: APPLICANT: Zilong Wen  
: APPLICANT: Curt M. Horvath  
: APPLICANT: Zhong Zhong  
: TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
: TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
: NUMBER OF SEQUENCES: 39  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Klauber & Jackson  
: STREET: 411 Hackensack Avenue  
: CITY: Hackensack  
: STATE: New Jersey  
: COUNTRY: USA  
: ZIP: 07601  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/369,796  
: FILING DATE: 06-JAN-1995

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-08-369-796-14

Query Match      14.5%; Score 112; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.4e-96;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SLSAEFKHLTLREQRCGNGGRNCDCASLIVTEELHLITFETEVYHQLKIDLETHSLPVPV 462
DB 1 SLSAEFKHLTLREQRCGNGGRNCDCASLIVTEELHLITFETEVYHQLKIDLETHSLPVPV 60

QY 463 VISNICOMPNAWASILWYNMLTNPKNVNFTKPPIGTWDQVAEVLWQFSS 514
DB 61 VISNICOMPNAWASILWYNMLTNPKNVNFTKPPIGTWDQVAEVLWQFSS 112

RESULT 19
US-08-852-091-14
; Sequence 14, Application US/08852091
; Patent No. 5983228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-08-852-091-14

Query Match      14.5%; Score 112; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.4e-96;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SLSAEFKHLTLREQRCGNGGRNCDCASLIVTEELHLITFETEVYHQLKIDLETHSLPVPV 462
DB 1 SLSAEFKHLTLREQRCGNGGRNCDCASLIVTEELHLITFETEVYHQLKIDLETHSLPVPV 60

QY 463 VISNICOMPNAWASILWYNMLTNPKNVNFTKPPIGTWDQVAEVLWQFSS 514
DB 61 VISNICOMPNAWASILWYNMLTNPKNVNFTKPPIGTWDQVAEVLWQFSS 112

RESULT 20
PCT-US95-17025-14
; Sequence 14, Application PC/TUS9517025
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17025
; FILING DATE: 28-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
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PCT-US95-17025-14

Query Match 14.5%; Score 112; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.4e-96;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 403 SLSAEFKHLTLREORCGNGGRANCDASLIVTEELHLITFETEVYHOGCLKIDLETHSLPVV 462  
DB 1 SLSAEFKHLTLREORCGNGGRANCDASLIVTEELHLITFETEVYHOGCLKIDLETHSLPVV 60  
QY 463 VISNICOMPNAWASILWYNMLTNNPKNVNFTKPPIGTWDQVAEVLWQFSS 514  
DB 61 VISNICOMPNAWASILWYNMLTNNPKNVNFTKPPIGTWDQVAEVLWQFSS 112

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Job time: 299 sec